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GenCore version 5.1.3
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OM nucleic - nu	nucleic search, using sw model
Run on:	January 3, 2003, 20:11:57 ; Search time 7402 Seconds (without alignments) 11712.680 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-842-484A-1 2979 1 ttataaactgattaaagaagacatttgcattttattaaaa 2979
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 segs, 14551402878 residues
Total number of	f hits satisfying chosen parameters: 4109280
Minimum DB seq Maximum DB seq	length: 0 length: 200000000
Post-processing:	<pre>g: Minimum Match 0% Maximum Match 100% Listing first 45 summaries</pre>
Database :	GenEmbl:* 11 9b ba:* 2 9b_htg:* 3 9b_htg:* 4 9b_om:* 5 9b_pt:* 6 9b_pt:* 10 9b_pr:* 11 9b_sts:* 11 9b_sts:* 11 9b_sts:* 11 9b_sts:* 11 9b_sts:* 12 9b_sy:* 13 9b_un:* 14 9b_vi:* 15 em_hun:* 16 em_fun:* 17 em_hun:* 18 em_nu:* 18 em_nu:* 22 em_ov:* 23 em_ov:* 24 em_ph:* 25 em_ov:* 25 em_ov:* 26 em_ov:* 27 em_sts:* 28 em_nu:* 29 em_vi:* 31 em_htg_nu:* 31 em_htg_nu:* 32 em_htg_nu:* 33 em_htg_nu:* 34 em_htg_nu:* 35 em_htg_nu:* 36 em_htg_nu:* 37 em_htg_vr:* 38 em_htg_vr:* 38 em_htg_vr:* 39 em_htg_vr:* 31 em_htg_vr:* 31 em_htg_vr:* 32 em_htg_vr:* 33 em_htg_vr:* 34 em_htg_vr:* 35 em_htg_vr:* 36 em_htg_vr:* 37 em_htg_vr:* 38 em_sy:* 38 em_sy:* 39 em_htg_vr:* 39 em_htg_vr:* 30 em_htg_vr:* 30 em_htg_vr:* 31 em_htg_vr:* 32 em_htg_vr:* 33 em_htg_vr:* 34 em_htg_vr:* 35 em_htg_vr:* 36 em_htg_vr:* 37 em_htg_vr:* 38 em_sy:*
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๙ No. is the number of results predicted by chance to have Pred.

Deaces 1 to 2979)
DeAngelis, P.L. and Padgett-McCue, A.J.
Identification and molecular cloning of a chondroitin synthase from Pasteurella multocida type F

Pasteurella multocida. Pasteurella multocida Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;

Pasteurella.

REFERENCE AUTHORS TITLE

BCT 07-AUG-2000

complete cds

AF195517 2979 bp DNA linear Pasteurella multocida chondroitin synthase CS gene,

GI:9716369

AF195517 AF195517.1

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 1
AF195517
LOCUS
DEFINITION

Dictyoste
Campyloba
Campyloba
Campyloba
Campyloba
Listeria
Human DNA
Clostride
Sequence
Sequence
Campyloba Campyloba Dictyoste Dictyoste Plasmodiu Dictyoste Dictyoste Campyloba Streptoco Dictyoste Trypanoso Streptoco Plasmodiu Pasteurel Botrytis Campyloba Pasteurel Pasteurel Pasteurel Pasteurel Pasteurel Nostoc sp Streptoco Streptoco Plasmodiu Trypanoso Campyloba Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AB079602 E AC007926 T AC116961 I AC116965 I AF400048 C AY044868 C AB012956 N AL591977 I AL391280 H AC081152 AP003187 C AX413863 S AX413863 S AX41529 C AF401529 C AF301528 C AB050723 AC116990 AC084397 AF349539 AL034556 AP003591 AF215659 AC114257 AC116923 AL034558 AC117080 AC115600 AC115600 AE006155 AX009404 AF448502 AL110675 AF130984 ALIGNMENTS SUMMARIES AX415777 AF401529 AF401528 AF343914 AB050723 AC116990 AC084397 AF349539 PFMAL3P5 AF067175 AF036004 AF237926 AB079602 AL391280 AC084152 CNS0180K AF130984 AF167344 AC114257 AC114257 AC116923 PFMAL3P2 AC117080 AC116101 В Length 9987 62352 171798 18239 86827 19966 27782 178273 11442 11455 16265 46721 270050 153026 54345 302000 12388 12390 15671 16563 10827 43993 Query Match 2979 2635.8 2632.6 2340.8 2283.4 2268.6 Š 0 0 0 0 0 0 0 0 0

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/note="polysaccharide-forming glycosyltransferase; similar
to pasteurella multocida type A hyaluronan synthase"
/codon_start=1
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/ref="di-
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                                                                                                                                          Biochem. & Molec. Biol., Univ. of Oklahoma 940 Stanton L. Young Blvd., Oklahoma City,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61. 2958
/function="synthesizes the chondroitin polymer backbone polysaccharide composed of repeating disaccharide units consisting of beta(1,4)glucuronic acid linked to beta(1,3)N-acctylgalactosamine) involved in capsule biosynthesis"
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/note="capsule type F
isolated from face lesion of
obtained from USDA"
61. 2958
                                                                      DeAngelis, P. L. and Padgett-McCue, A.J. DeAngelis, P. L. and Padgett-McCue, A.J. Direct Submission Submitted (15-OCT-1999) Biochem & Mo Health Sciences Center, 940 Stanton LOK 73104, USA
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.larity 100.0%; Pred. No. 0;
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                         GTTCTTGCTCCATTGCCAGATCATGTTAAATGATTTTACATGGTACAAAAAATCGAAAAAAA
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AE006116 11885 bp DNA linear BCT 08-MAR-2001
Pasteurella multocida PM70 section 83 of 204 of the complete
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                                                              GCGCATCCACCATTTAAAAAGCTGATTAAAACCTATTTAATGACAATGACTTAAGAAGT 2640
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2 hang, Q, and Kapur, V.
Direct Submission
Submitted (24-OCT-2000) Department of Veterinary Pathoblology, University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN 55108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pasteurella multocida.
Pasteurella multocida
Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
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1 (bases 1 to 11885)
May, B.J., Zhang, Q., Li, L.L., Paustian, M.L., Whittam, T.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete genomic sequence of Pasteurella multocida, Pm70 Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (2001) 21145866
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .11885
/organism="Pasteurella multocida"
/strain="PM70"
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205. .2073
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Pasteurella multocida P4218 region 2 capsule biosynthesis gene cluster, partial sequence.

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699. .2567
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Thorseal, K. M., Boyce, J.D., Chung, J.Y., Frost, A.J. and Adler, B. Direct Submission

Submitted (03-SEP-2000) Veterinary Pathology and Anatomy, The University of Queensland, School of Veterinary Science, Brisbane, QLD 4073, Australia

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  Adler, B.
                                                                                                                                                                                           Pasteurellaceae;
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Loci
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Townsend, K. M., Boyce, J.D., Chung, J.Y., Frost, A.J. and Genetic organization of Pasteurella multocida cap Loci development of a multiplex capsular PCR typing system J. Clin. Microbiol. 39 (3), 924-929 (2001)
                                                                                                                                                                                           gamma subdivision;
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complement(<1, .351)
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Pasteurella.
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ATGTAGAATTTGGTTACAGATTATTTGCCAAAGGCTGTTTTTCAGAGTAATT. 12. 	AATGGCCATCCATCAAGAACCACCTGGTAAAGAAAATGAAACAGAACGCGAA 1 	paaagtattacgcttaaaattgtgaagaagaaaggtaccttacatctatagaaag 13 	CCAATAGAAGATTCACATATTCATAGAATACCTTTAGTTTCTATTTATATCCCC 13 	TIGTGCAAATTATATTCAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTT 1. 	GAGGTTTGTATTTGTAACGATGGTTCAACAGATAATACCTTAGAAGTGATC 1. 	Tratggtaataatcctagggtacgcatcatgtctaaaccaaatggcggaata 1: 	DARATGCAGCCGTTTCTTTGCTARAGGTTATTACATTGGGCAGTTAGAT 1	TTGAGCCTGATGCAGTTGAACTGTGTTTAAAAGAATTTTTAAAAGAT 1. 	CTAGCTTGTGTTTATACCACTAATAGAAACGTCAATCCGGATGGTAGCTTAATC 1 	STTACAATTGGCCAGAATTTTCACGAGAAAAACTCACAACGCTATGATTGCT 	TAGAATGTTTACGATTAGAGCTTGGCATTTAACGGATGGAT	CCGTGGGTTATGACATGTTCTTAAACTCAGTGAAGTTGGAAAATTTAAA 	AAAATCTGCTATAACCGGTATTACATGGTGATAACACATCCATTAAGAA 	daaagaaaaccatttgttgttgtagtcaatcagtcattaaatagacaagc 	rattataattatgacaaatttgatgattagatgaagtagaaagtatatett 	CTGAATATCAAGAAAAGGATATGTTAAAAGATCTTAAACTCATTCAA 	SCCAAAATCGCAGTCACTATTTCTATCCCAATACATTAAACGGCTTAGTG	CAATAAU IATATA CAAATATA COTTATTATTATTATTATTATTATTATTATTATTATTATTA
GCGAAG GCGAAG	GACGGCGG GACGGCGG	961	CTTTTACC	CTTATA CTTATA	0-0	AAGC AAGC	GCCTCAG GCCTCAG	4-8	AAAACGC AAAACGC	GCTAATG GCTAATG		ATTGAAAACG	5 - 5	CTCGGC/ CTAGAC/	CAAT AAGT	AATAAAACCG	AA'	
1141 G 3664 G	1201 G	1261 C	1321 0	381	41 64	501	561 084	7	1681	1741		38		98	2041	2101	16	4684
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AF067175 1000 16727 bp DNA linear BCT 05-MAY-2000 pasteurella multocida capsule biosynthesis gene cluster, complete
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Pasteurella multocida
Bacteria; Pototeobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
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The capsule biosynthetic locus of Pasteurella multocida A:1'
FEMS Microbiol. Lett. 166 (2), 289-296 (1998)
                                                                                                                                                                                                                                        AACACTGAGGATATTTGGTTCCAATTTGCACTTTTAATCTTAGAAAAGAAAACCGGCCAT
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                               4804 GACAAAAATCATCTCACATCAACATCAAAAGGAAATACTAGAATTTCATAACAAGAAT
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2 (bases 1 to 16727)
Chung,J.Y., Zhang,Y. and Adler,B.
Direct Submission
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TLPPIHEYEDAHEANRIKSHLSYKLGVLFLQEINNPFKWLTLPYKLIKEGKRFKQG"
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Submitted (19-MAY-1998) Microbiology, Monash University, Wellington Road, Clayton, VIC 3168, Australia 3 (bases I to 16727) Chang, V. Zhang, Y. and Adler, B. Direct Submission Submitted (05-MAY-2000) Microbiology, Monash University, Wellington Road, Clayton, VIC 3168, Australia Sequence update by submitter on May 5, 2000 this sequence version replaced gi:3435183.
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DRSEGKKVAAGKLGDFLVPLQYLDDSQYRTHCDYESYDAFLKEILESFIHHAPSALN
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VWGHSHIEVVEYAKQQQLPLLRMEDGFLRSVGLGSNLTPPISLVLDDVGIYFDAQSR
SRLEDILQHQSFTLKDLQRAETLKKTLIEQHIGKNVGHTHCLTHIRDRNKLLVVGV
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DFVVEKIVILDCIIVVDEVHYMTSLAGFEALLREKKHGYGYGLPFYSNMGLTVDHLSCH
RRSRKLSLLELIAGVLIYYPQYIDPKTKTMIDVQRAVDLLIEQRRKIKNNKLHTNYFM
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LMLANIEQNFWGWSDPNAIQILDYWANLDPNIHFVFVYDKPENLFQYHSLEEALKLDK
HTVQEKFEEWQTYNEKILTYFNKYKDRSVLLNTQQLQNTKKTSLSEIYKHISAPDALV
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KINFNSGDEAFYPNSIPQTFAYQGQLDQFDQYLRFFCHQHSIDAIICFGDTRAYHRIA
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XIDTOHIDPKDFLNNASLLESLPEVKTNNSVAAKGEGTVSLDWRLEQFEKTENLERLS
SPERFEAGRVAFAKKWLKSGFEDEENHWGEDVEGTVRLEWGEFKTTOGIMA
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VEKENSKKLENINQFLYFYRGEITTIKTEDPPNTNNIVSHSMVNDTNTYLNAPLITI
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Pasteurella multocida
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
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a unique hyaluronan
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y functional expression
                                                                                                                             TTAGAAAAGAAAACCGGCCATGTATTTAATAAAACATCGACCCTGACTTATATGCCTTGG
                                                                                                                                              ATTGATAGTGTGCCAGAATATAACACTGAGGATATTTGGTTCCAATTTGCACTTTTAATC
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DeAngelis,P.L., Jing,W. and Achyuthan,A.M.
Direct Submission
Submitted (26-NOV-1997) Biochem. 6 Molec.
Health Sciences Center, 940 Stanton L. You
OK 73104, USA
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/organism="Pasteurella multocida"
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/db_xref="taxon:747"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="polymerizes hyalurona
hyaluronic acid) polysaccharide
hyp-GicNAc precursors:
/note="glycosyltransferase; HA s:
membrane-bound enzyme"
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DeAngelis, P.L., Jing, W., Drake, R.R. and A. Identification and molecular cloning of a synthase from Pasteurella multocida J. Biol. Chem. 273 (14), 8454-8458 (1998) 98192645
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21; Length Indels DB 1; 376; Score 2283.4; Pred. No. 0; 0; Mismatches б 509 Query Match 76.6%; Best Local Similarity 86.5%; Matches 2540; Conservative O 482 ಡ 1077 BASE COUNT ORIGIN

Gaps

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540 900 681 999 741 CATGTTAATGATTTTACATGGTACAAAAGCGAAAGAAAAGACTTGGCATAAAACCTGAA 480 441 420 561 621 209 180 261 240 300 381 360 501 162 321 9 AATAAGAATATCGGTCTTTCTATTATTATTCCTACATTTAATCGTAGCCGTATTTAGAT GATGATGGTAGTAAGGAAAACTTACTTACCATTGTGCAAAAATACGAACAAAAACTTGAC CATGITAATGATTTACATGGTACAAAAATCGAAAAAAAAAGCTTAGGTATAAAGCCTGTA ATAACGTTAGCCTGTTTGGTCAATCAGAAACAAACTACCCATTTGAAGTCGTTGTTGCA ATTACATTAGCCTGTTTAGTAAACCAAAAAACACATTACCGTTTGAAGTTATGGTGAGA ATTTTAAAGGAAAGAAATGAATACATTATCACAAGCAATAAAAGCATATAACAGCAAAT **AGTITIAAAAAATAAATGGAAATCTATCACTGGGAAAAAATCGGAGAACGCAGAAATCAGA** GACTATGAATTAGCACTCAAATTATTTGAGAAGTCTGCTGAAAACCTACGGGCGAAAAATC -----TTATGTAAGTGAAGATAAAAAAAAAGTGTTTGCGATAGCTCATTAGATATC 541 502 622 601 682 181 241 322 301 382 442 421 481 562 43 103 61 163 121 210 262 361 QY Db Oy Oy Oy Oy Db Qy g δλ qq Ω g 90 yo Dp ò g Ωÿ

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YHQEPPGKENETDREAGKNITLDIMREKVPYIYRKLDFIEDSHINNVPLVSIYIPAN
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SASNAAVSFAKGYIGQLDSDDYLEPDAVELCIKEFLKDKTLACVTTNRNNNPDGSL
IANGYNWPESPERKLITAMAAHHFNPTIRAMHLTDGFNEKIENAVDDMFKLESUG
KFKILNKICYNRULHGDNTSIKLGKNNITLDEPNEKIELNESV
KKXILNKICYNRULHGDNTSIKLGKNNITLESVNKI
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SQUINNGET II IBONHDSLEVKRUSYAYMKKYDYGMRFSALTHDWIEK INAHPPEKKLI
KTYENDIDIK SMNYGASQOMHTVALAHELLI II KEVITSOQSIDSYPEY PEDIWE
OFALLILEKKTGHVFNKTSTLTYMPWERKLQWTNEQIESAKRGENIPVNKFIINSITL
                                       2919 bp DNA linear BCT 08-MAY-2000 hyaluronan synthase (has) gene, complete cds.
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Fuller, T.E., Kennedy, M.J. and Lowery, D.E.
Direct Submission
Submitted (24-FEB-2000) Discovery Research, Pharmacia & Upjohn
Animal Health, 7923-25-434, 7000 Portage Road, Kalamazoo, MI
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Pasteurella multocida

Bacteria: Proteobacteria: gamma subdivision; Pasteurella.

Pasteurella.

[ bases 1 to 2919)

Fuller, T.E., Kennedy, M.J. and Lowery, D.E.
Identification of Pasteurella multocida virulence genes septicemic mouse model using signature-tagged mutagenesi.
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/organism="Pasteurella
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GAAGATAAAAAAAAGGTGTTTGCGATAGCTCATTAGATATCGCAACACAGCTCTTACTT 	TCCAACGTAAAAAAATTAACTCTATCCGAATCAGAAAAAAAGGTTTAAAAAATAATGG 	AAATCTATCACTGGGAAAAATCGGAGAACGCAGAAATCAGAAAGGTGGAACTAGTACCC	AAAGATTTTCCTAAAGATCTTGTTCTTGCTCCATTGCCAGATCATGTAATGATTTTACA	TGGTACAAAAAATGGAAAAAAAGCTTAGGTATAAAGCCTGTAAATAAGAATATCGGTCTT 	TCTATTATTGTTCCTACATTTAATCGTAGCCGTATTTTAGATATAACGTTAGCCTGTTTG 	GTCAATCAGAAACAAACTACCCATTTGAAGTCGTTGTTGCAGATGATGGTAGTAAGGAA 	AACTTACTTACCATGGGAAAAATACGAACAAAAACTTGACATAAAGTATGTAAAGACAA 	AAAGATTATGGATATCAATTGTGTGCAGTCAGAAACTTAGGTTTACGTACAGCAAAGTAT 	GATTITGECTCGATTCTAGACTGCGATATGGCACCACAACAATTATGGGTTCATTCTTAT	CTTACAGAACTATTAGAAGACAATGATATTGTTTTAATTGGACCTAGAAAATATGTGGAT 	ACTCATAATATTACCGCAGAACAATTCCTTAACGATCCATATTTAATAGAATCACTACCT	GAAACCGCTACAAATAACAATCCTTCGATTACATCAAAAGGAAATATATCGTTGGATTGG 	AGATTAGAACATITCAAAAAACCGATAAICTACGTCTATGTGATTCTCCGTTTCGTTAT	TITGITGCGGGTAATGITGCATTITCTAAAGAATGGCTAAATAAAGIAGGTIGGTICGAT 	GAAGAATTTAATCATTGGGGGGGGGGAGATGTTAGATTTGGTTACAGATTATTGCCAAA 	GGCTGTTTTTCAGAGTAATTGACGGGGAATGGCCATCCAT	Garartgaracagarcgcgargctggtarargtattacgcttararttgtgraragararag
220	280	340	400	460	520	580	640 601	700	760	820	880	940	1000	1060	1120	1180	1240
Qy Dp	QY	Qy	Qy Db	O.y D.b	QY	Qy Db	Oy Db	Qy Dp	Qy Db	Qy	Qy	Qy Dp	Qy Db	Qy	Qy Db	Qy	Qy Db

2340 1419 1479 1539 1500 1599 1620 1680 1779 1740 1800 1899 1860 1959 1920 2019 1980 2079 2040 2139 2100 2199 2160 2259 2220 2319 2379 2439 1659 1719 1359 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCACATATTCATAGAATACCT GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGCATCATG 1621 TTAAAAGAATTTTTAAAAGATAAAACGCTAGCTTGTGTTTTTTAAAATAGAAACGTC GAAAGTAGAAACTATATCTTCAATAAAACCGCTGAATATCAAGAAGAAATGGATATGTTA TTGGCTTTCTATCATAAGCACCAAGTGAATATTTTACTAAATAATGACATCTCATATTAC ACGAGTAATAGACTAAATAAAAACTGAGGCACATTTAAGTAATATTAAATTAAGTCAG AATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTGGCCAGAATTTTCACGAGAAAAA CTCACAACGGCTATGATTGCTCACCATTTTAGAATGTTTACGATTAGAGCTTGGCATTTA CAGTCATTAAATAGACAAGGCATCAATTATTATAATTATGACAAATTTGATGATTAAGAT TTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGTAGAT TTAAAAGAATTTTTAAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTC AGTGAAGTTGGAAAATTTAAACATCTTAATAAAATCTGCTATAACCGCGTATTACATGGT GATAACACATTTAAGAAACTCGGCATTCAAAAGAAAAACCATTTTGTTGTAGTCAAT 1420 1540 1561 1780 1840 1801 1861 2020 1981 2080 2041 2140 2101 2200 2260 2281 1720 1900 1960 2161 2221 2320 2380 1360 1480 1441 1600 1681 1921 1300 1261 1321 1381 1501 1660 1741 qq Op δy qq qq qq Op g οy QΩ δλ qq δλ Op g δ g Op Dp δy Dp δy Pp Qγ Dβ Qγ qq οy οğ δý QY δλ Qγ δ Ω Qγ QΥ

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Direct Submission
Submitsed (07-FEB-2002) Nobuo Suglura, Aichi Medical University,
Institute for Molecular Science of Medicine; 21, Yazako, Nagakute,
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URL http://www.laichi-med-u.ac.jp/imsm/index-e.html,
Tel81-52-264-4811(ex.2087), Fax:81-561-63-3532)
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14483 bp DNA linear BCT 11-JUN-200 Escherichia coll kpsS, kfo6, kfo6, kfo7, kfo1, kfo1, kfo1, kfo2, kfo6, kfo8, kfo8, kpsS hypothetical protein, predicted glycosyltransferase, UDP-glucose dehydrogenase, KfoE hypothetical protein, IS hypothetical protein, IS hypothetical chondroitin polymerase, kfoB hypothetical protein, IS hypothetical protein, ehondroitin polymerase, kfoB hypothetical protein, and the statement of th
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Molecular Cloning and Characterization of Chondroitin Polymerase
from Escherichia coli Strain K4
J. Biol. Chem. 277 (24), 21567-21575 (2002)
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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2920 CCCGTTAACAAGTTCATTAATAGTATAACGCTATAA 2958
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/product="UDB-glucose 4-epimerase"
/protein_id="BAC00525.1"
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HTG 17-JUL-2001
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El-Sayed,N.M., Ghedin,E., Song,J., Larkin,C., Wanless,D., Jones,K., Peterson,J., Hou,L., Zhao,H., Mason,T., Millischer,J., Pal,G., Van Aken,S., Utterback,T., Khalak,H.G., Gerard,C., Leech,V., Ullu,E., Melville,S., White,O., Adams,M.D., Donelson,J.E. and Fraser,C.M. Trypanosoma brucei GUTatio.1 RPC193-3H15 BAC genomic sequence
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El-Sayed, N.M., Khalak, H. and Adams, M.D.

El-Sayed, N.M., Khalak, H. and Adams, M.D.

Direct Submission

Submitted (28-JUN-1999) The Institute for Genomic Research, 971:

Medical Center Dr., Rockville, MD 20850, USA

On Jul 17, 2001 this sequence version replaced gi:12746529.

* NOTE: This is a "working draft' sequence. It currently

* consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* This sequence as soon as it is available and

* the accession number will be preserved.
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                                                                                                                                                      1848 ATTTAACGAAAATATTGAAAACGCCGTGGATTATGACATGTTCCTTAAACTCAGTGAAGT
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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1 (bases 1 to 100726)
Gloeckner.G., Elchinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K.,
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
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HVIMENDLIADYRYKINQTSTNDLILSSSLQLSMGVCLTLLIGNGVSSIFRGDPNFGV
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                                                                                                 Baumgart, C.
Direct Submission
Submitted (21-MAY-2002) Genome Analysis, Institute of Molecular
Submitted (21-MAY-2002) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
CDS predictions from GeneID may contrain errors. Further Information
is available from IMB Jena, Department of Genome Analysis
(http://genome.lmb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Biochemistry I
Chttp://www.uni-koeln.de/dictyostelium/project.shtml
Funding
                         Molecular
                                                                                                                                                                                                                                                                                                                    Agency: Deutsche Forschungsgemeinschaft (DFG).
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
1. 100726
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/note="ORF_ID;dd_02644"
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Direct Submission
Submitted (04-APR-2002) Genome Analysis, Institute o:
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
3 (bases 1 to 100726)
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Pred. No. 5.3e-05;
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COMPIEMENT (15000 . 15245)
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NNFNKVYDAVPERLYVLEDKKFKYVGCPGPFGFIPEELREFLTKRYKPKPHLLDLKNNLS
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FCPRELLLSATNIAMDSLHNASKRIKEEKDTYNQLPTESIIKLNERINREIILKEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-MAY-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis
                                                                                                                                           AC116965 HTG 18-MAY-2002 Dictyostelium discoideum chromosome 2 map 497421-541412 strain AX4, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 4399)
Glockher, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P.,
Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K.,
Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Bentenberstr. 11, Jena 07745, Germany 3 (bases 1 to 43993)
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://genome.imb-jena.de/dictyostellium/)
and the Univerity Colonge, Institute for Biochemistry I
(http://www.uni-koeln.de/dictyostellum/project.shtml
Sequence and Analysis of Chromosome 2 of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Dictyostelium Genome Sequencing Consortium 2 (bases 1 to 43993)
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                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum Dictyostelium discoideum
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LNSGAKVFWADFEDANCPNRENSIHOOOMIONNRTISFTSABGRKYELNKOVAVLF
VRRGWHLNRDHLATDCLSWSGSLEDFGCYTFHNGJILKNRNSNPYFYLPKMSSHLEA
RLWNDVFVFSONYLGMPIGTIKATVLIETILASFEMDEILYELRDHSAGLNCGRWDXI
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nnnndidetnebekkktgefeggeberekerekerkreknennnn
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KEFEIDYKFTGYLDAVKSALEPKQTEIKTTKTTPTFTTTKTVTKKIVKSK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IKQASPILIYSILFTGWKHARFMILPALALLLPQVYDFSVVDISKVKKV"
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Join (2230) 0. 22375,24040. 24056)
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LVLISTSHDEGLCYVETSNLDGETNLKVRRALGDTNKLSTAEDISLLRGSIVYETPNE
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COMPLEMENT (24572. . .24778)
/note="ORF_id;dd_01216"
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FRKSSRDYRLSIGSIGSSNMESILNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNDDN
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FSFIKKFQSYPDKMLPDRAKVTMTSPFMDSYVKLLIYTCHKRGVHAMGGMAAQIPIKN
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Pred. No. 0.00025;
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AF4,00048 I1442 bp DNA linear BCT 03-JAN-2002 Campylobacter jejuni strain AFCC 43438 heptosyltransferase I (waaC) gene, partial cds; lipid A biosynthesis acyltransferase I (waaC) putative two-domain glycosyltransferase, putative glycosyltransferase, beta-1,4-N-acetylgalactosaminyltransferase (cgtA), beta-1,3-galactosyltransferase (cgtB), alpha-2,8-sialyltransferase (cgtB), alpha-2,8-sialyltransferase (cstII), putative sialic acid synthase (neuBl), putative N-acetylglucosamine-6-phosphate 2-epinerase (neuBl), CMP-NeuSAc synthetase (neuAl), putative acetyltransferase, and putative glycosyltransferase genes, complete cds; and heptosyltransferase II (waaF) gene, partial cds.
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Michniewicz,J., Cunningham,A.M. and Wakarchuk,W.W.
The Genetic Bases for the Variation in the Lipo-oligosaccharide of
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FEATURES

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Glibert, M., Karwaski, M.F., Bernatchez, S., Young, N.M., Taboada, E., Michniewicz, J., Cunningham, A.M. and Wakarchuk, W.W.
The Genetic Bases for the Variation in the Lipo-oligosaccharide of the Mucosal Pathogen, Campylobacter jejuni. BIOSYNTHESIS OF SIALYLATED GANGLIOSIDE MIMICS IN THE CORE OLIGOSACCHARIDE J. Biol. Chem. 277 (1), 327-337 (2002)
                                                                                                                                                                                                                                             Campylobacter jejuni
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
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Gilbert, M., Michniewicz, J., Karwaski, M.-F., Cunningham, A. and
Wakarchuk, W.W.
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Submitted (10-JUL-2001) Institute for Biological Sciences,
Research Council of Canada, 100 Sussex Drive, Ottawa, Ontar
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9053. 9718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1356 ACCTTTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGT 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGGTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCACATATTCATAGAAT 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAT - - - GTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="orfll; premature translational stop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative acetyltransferase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variation in homopolymeric G-tract"
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Pred. No. 0.00037;
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                                                                                                                                                                                                                                                                                           9053. .9718
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SKETLKKIFLTLF"
complement (5044. .5949)
/gene="cgtb"
complement (5044. .5949)
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ICNTKNEVLYKNNIQELQLVLNYLRQNYILNKYCSVLYVLIKYLLYIQIYKIKRM
6038 6913
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NFIELAPNLNSNFIIQEKNNYTKDILIPSSEAYGKFTKNINFKKIKIKENIYYKLIKD
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YSKSKSYILLIDGDMILEKPYRTKNHEPREFAKRKVILQGSRIILNEKESEEILKNDNYSL
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                                                                                                                                                                                                                                                                                                                                                                                                                     KNVDVLWFDHDCTYEDNIKNKHKKTRMEIFNFKEECIITPKEYANRALSVGSRDISFG
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beta-1,4-N-acetylgalactosaminyltransferase"
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4015.,5058
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/note="orf4"
                                                                                                                                     NKKISWR"
2773. .3
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4015. .
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/ ..._..... dililings.
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// DLFSAKLEILNSSKLFFEYLLSGEFFKLNTOKVFKDIK"
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KQEQVTIDFAFASVVSIKDIKKGEVLSMDNIWVKRPGLGGISASEFENILGKKALRDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="orf11; premature translation stop due to deletion in homopolymeric G-tract"
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                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative N-acetylglucosamine-6-phosphate"
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Pred. No. 0.00037;
0; Mismatches 196;
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7951. .9069
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                                                                                                                                                                                                                                                                                                                      galactosyltransferase; mannose-1-phosphate guanylyl transferase;
ORF21x9 gene; ORF34x7 gene; ORF35x9 gene; ORF39x2 gene; ORF40x0
gene; ORF40x1 gene; ORF41x3 gene; ORF41x8 gene; ORF41x9 gene;
ORF50x8 gene; ORF54x5 gene; ORF56x5 gene; oxido-reductase; Rfc-like
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ANDVAMGTRALLAF RELLGLEKTTRENGSTSELYGLVGETPGKETTPFYPRSPAVA
KMYAVWIVVNYRESYGMYACNGILFNHESPRRGETFVTRKITRGLANIAGGLEKCLYM
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EGGGVDEKGIVTAIEGDKAPALKVGDVVVQIDPRYFRPAEVETLLGDPSKAKQKLGWT
                                                                                                                                                                                                                                         BCT 30-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-SEP-1996) P.A. Manning, University of Adelaide, Dept of Microbiology and Immunology, GPO Box 498, Adelaide S A 5005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
1 (bases 1 to 16265)
Manning, P.A.
                        Revised by submittor 20-OCT-1996
2 (bases 1 to 16265)
2 Stroeber,U.H., Parasivam,G., Dredge,B.K. and Manning,P.A.
Novel Vibrio cholerae 0139 genes involved in lipopolysaccharide biosynthesis
1593 TAMAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGA 1652
                                                                                                                                                                                                              V.cholerae ORF's involved in lipopolysaccharide synthese. Y07786 Y07787 Y07786. Y07880
                                                                                                              Db 11049 AATAGCGTTTAAAGAGATGAAAAAGGTTTTGATTGCTTTGTTTTGATGCC 10998
                                                                                     1653 ACTGTGTTTAAAAGAATTTTTAAAAGATAAAACGCTAGCTTGTGTTTATACC 1704
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Vibrio cholerae.
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VCLPSS
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KEYWORDS
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JOURNAL
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8852. 9865
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10797. .11861
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7398. .8855
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1330 ATAGAAGATTCACATATTCATAGAATACCTTTAGTTTCTATTTATATCCCCGCTTATAAC 1389

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YCLDREIPFLYASSAATYGETOFFIEEPQYEGALNVYGYSKQOFDNYVRRLWIDAKOH
DETLSQITGFRYFNVYGPREQHKGSMASVAFHLNNQMNAGENPKLFAGSENFKRDFVY
VGDVAAVNIMFLDHGYSGIFNGGTGRAESFNEYAKAVIAFHGRGEVETIPFPDHLKGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamasaki,S., Shimizu,T. and Hoshino,K.
Yamasaki,S., Shimizu,T. and Hoshino,K.
Direct Submission
Submitted (14-APR-1998) Shinji Yamasaki, Internatinal Medical
Center of Japan, Research Institute; Toyama 1-21-1, Shinjuku, Tokyo
162-8655, Japan (E-mail:shinji@ri.imcj.go.jp, Tel:+81-3-3202-7181,
Fax:+81-3-3202-7364)
                                                                                                                                                                                                                                                                                                                                                                                                                           vibrio cholerae genes for O-antigen synthesis, strain MO45, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamasaki,S., Shimizu,T., Hoshino,K., Ho,S.T., Shimada,T., Nair,G.B. Yamasaki,S., Shimizu,T., Hoshino,K., Ho,S.T., Shimada,T., Nair,G.B. The genes responsible for O-antigen synthesis of vibrio cholerae 0139 are closely related to those of vibrio cholerae 022 gene 237 (2), 321-332 (1999)
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                                                                                                                                                                                                       1510 TATGGTAATAATCCTAGGGTACGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCA 1569
                                                                                                                                                                                                                                         9014 ATGAAGAAGGATGACCTATTGTATTGGTTTCAAGAGAAAACAAAGGCTAATAGTAAGC 9073
                                                                                                                                                                                                                                                                                      1570 ICAAATGCAGCCGTTTCTTTGCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGAT 1629
                                                                                                                                                                                                                                                                                                           8834 ATATAAGGIGGTTTTAAAATGAGTICACCAAAAATATCGGTTGTTATGTCTTTATAAT
                                          TGTGCAAATTATATTCAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTC
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB012956.1 GI:3724295
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JOURNAL
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MEDLINE
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AB012956
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KEYWORDS
SOURCE
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NITVEIRGEWNERPAYYENKSTEETYODIIKMAGGETANAYRDKTEVKRYASDGIRKALTL.
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INGEVQVPYTYLLDSGLNVODYLNKAGGVKKQADADRIFKR
18485. . . 19492
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GLKFSEVRQSLGQRVEEQMIGIRSDISLGELRTWQIFVWGDAYKPGAYTVSALTTLSQ
AIYYSGGFSQSGALRNIQLKREGQLVVQLDLYDLLLKGDNRNDVRLMPGDVVFIGAVD
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FDGSSYSTQEKSHGRIETRVALVNRDLSVLGDIEHEWPGLKSMGIVASIRQESAVATE
QDVSIRYYICSKELEAQTLLEATRSHWGVEVNHWSLDTAFCEDNSRIRADDRAEAFAR
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15645. 18380
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20961. .22079
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18485, 104
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19650. .20777
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                                                                 /note-"unknown"
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                                                                                                                      TAYERTNQDVIQNLFSFKFRATNALGSLGQEIDLDIDIDQRDTPWTVPSDVELSSAQLF
YDGKQFNAPYALMOSLNTSSEDKYSYSNLINVDNYYLKIKGKEISPPSSPYWKFQHV
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ETFLYQYQDLKKRTLGSELIDPSIDNIPLLKNISAQODQQDLLKRQPYWWLEE"
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14390. .14638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALSYLY77 270050 bp DNA linear BCT 06-JUN-2002
Listeria monocytogenes strain EGD, complete genome, segment 5/12.
ALS91977 ALS91824
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                                                                                                                                                                                                                                                                                                                                                                                    1510 TATGGTAATAATCCTAGGGTACGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCA 1569
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                                                                                                                                                                                                                          1390 TGTGCAAATTATATTCAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTC 1449
                                                                                                                                                                                                                                                                                                       1450 GAGGTTTGTATTTGTAACGATGGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTT 1509
                                                                                                                                           1330 ATAGAAGATTCACATATTCATAGAATACCTTTAGTTTCTATTATATCCCCGCTTATAAC 1389
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Listeria monocytogenes
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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0
                                                              Length 46721;
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E-mail: pglaser@pasteur.fr
Phone: +33 1 45 68 89 96, Fax: +33 (0)1 45 68 87
Location/Qualifiers
1. 270050
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                                                                                                      0; Mismatches 136;
                                                           Score 82.4; DB 1;
Pred. No. 0.00026;
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Microorganismes Pathogenes, 25 rue du
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1277. .1831
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ILIYPHEETLLLGNINGDFRQLFFGKSEAAEIYPLEIRAEAGGTSFITNWEPELEIFV
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VENLIIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAC98935.1"

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//db xref="SPTREME.:03878"

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PVFEHIEIPTFIAGGSADQVVPAEKSVNFLMESIPGFKELFILLEGSKHVICQDEQADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref-"SPTREMBL:0818P0"
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LESLALKTIPIGTGYAIWTGIGAVGSVTLGMIVFKERKSVGKLLFITMIIAGVVGLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to transcription regulator lacI family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="UDP-N-acetylmuramoylalanyl-D-glutamyl-2,
6-dlamino pimelate-D-alanyl-D-alanyl ligase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(5990. .7028,7035. .7040))
/gene="lmo0858"
                                                                                                                                                                                                                                                                                                                               /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to carboxylesterase"
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       // 2011/2050 ...3774,3788 ...3822)
// gene="ddlA"
2650 ...2655
// gene="ddlA"
2662.
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/gene="lmo0857"
5263. .5268
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// gene="ddlA"

| foin (3822. 3828, 3838. 5211)

// gene="murF"

3822. 3828
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/gene="lmo0858"
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/gene="lmo0857"
5278, .soo
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5998. Ano
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3838. ...
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EEAATNQLEPEQLTSEWATGIFLLSHINTDYSKKVIDLGMPVVLLDHHDPHLKADAVIS
WINGGAFMAVEFLIONKHQKIGFLGOVFSPSYEERLEGYKKALQYYHIPFNKKYAIT
RIKEEQTTLYRTLDELDELPFAWFCVNSGLGFILNTVLQSKGYNIPROLSIICEDNTE
FTVLSNPQLTTWCTNLSFMGEKAVELMYNRIRKPDEGFVHLALATNLIARDSVGENKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 234478 ATTCTTTTGGAACCTTTAGTAAGTGTAATTATTCCAGTTTATAATGTAGAAAAGTATGTT 234537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 234652 CGAATTCGTTATTTGAAAAAGAAAATGGCGGACAAGCTACTGCCCGAAATTTGGATTA 234711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 234712 GATGTGGCTACGGGAGATTACATCGTGATGGTAGATAGTGATGATTACATTAGCAAAAAC 234771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1345 ATTCATAGAATACCTTTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATT 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGT 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGGTACGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTT 1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1585 TCTTTTGCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGAT 1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 234538 AAACGATGCTTGGATTCAGTTCTTGAGCAAACATATCATAACCTCGAAGTTATCGTAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACGATGGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCT
                                                                                                                                                                                                                                                                                                                                                                                          Length 270050;
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                                                                                                                                                                                                                                                                                                                                                                                          2.8%; Score 82.4; DB 1; Length 27 ilarity 55.0%; Pred. No. 0.00017; Conservative 0; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 234772 CTAGTAGAAACTTGTTTGGATACTGTACAAAAAAGGAA 234809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1645 GCAGTTGAACTGTTTTAAAAGAATTTTTAAAAGATAA 1682
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Job time: 8776 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Best Local Simi
Matches 186;
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BEST AVAILABLE COPY

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

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Database

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Streptococcus poly
Human immune syste
Chemically treated
Human immune syste
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Tumour suppressor
Human immune syste
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Human angiogenesis
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Human immune syste
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Plasmodium falcipa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chondroitan synthase; CS; enzyme; hyaluronic acid; ulcer; tissue abrasion; viscoelastic replacement; bloadhesive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P. multocida chondroitan synthase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                        AAA53720
ABL34358
ABL33432
                                                            AAS63332
AAA70106
ABN67436
ABL34155
AAT62328
                                                                                                                                                                                                                                                                                                                                                                      AAS61386
ABL32484
AAZ45260
AAZ30357
ABQ67858
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ABL34072
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ABL33142
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ABL32299
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61..2958
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA27449 standard; cDNA; 2979 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "PmCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US26501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0107929
99US-0283402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (OKLA ) UNIV OKLAHOMA STATE
  (first entry)
 Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200027437-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-NOV-1998;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAY-2000
AAA27449;
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AAA27449
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Pasteurella multoc
Pasteurella multoc
P. multocida hyalu
P.multocida hyalur
Enterococcus faeca
Listeria monocytog
Listeria monocytog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P. multocida chond
                                                                                   ; Search time 574 Seconds
(without alignments)
11687.636 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                 1. (SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2. (SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3. (SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
4. (SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
5. (SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
5. (SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
6. (SIDS2/gcgdata/geneseqn-embl/NA1981.DAT:*
7. (SIDS2/gcgdata/geneseqn-embl/NA1992.DAT:*
                                                                                                                                                          1 ttataaactgattaaagaag.......acatttgcattttattaaaa 2979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
            GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                       2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                     ٠.
                                                                                                                                                                                                                                                                                                                                  Listing first 45 summaries
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ABA05098
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AAX35589
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AAX13074
ABQ68041
ABQ69955
                                                            - nucleic search, using sw model
                                                                                   January 3, 2003, 20:10:07
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                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                      seq length: 0
seq length: 200000000
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2979
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Match
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99.5
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99... 1111... 1123... 1144... 1174... 1199... 120... 120... 120... 120...

2979 2979 2283.4 2283.4 1503.2 86 81

126459786

Score

Result Š.

or

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The present sequence is the coding sequence of the Pasteurella multocida chondroitan synthase PmCS. PmCS catalyses glycosaminoglycan polymerisation to produce chondroitan: a linear polyaccidaride which has viscoelastic properties which makes it useful for a number of applications. Chondroitan can be used with hyaluronic acid (HA) to coat medical devices e.g. catheters and sensors to reduce tissue abrasion. In addition, they can be used as bloadhesives for haemostatic sealing and healing of wounds and surgical incisions; and as biomaterials that provide sustained delivery of encapsulated drugs, to wounds, ulcers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GITCITGCICCATIGCCAGAICAIGITAAIGAITITACAIGGIACAAAAAICGAAAAAA 480
                                                                                                                                                                                                                                                                                   Gaps
                                              I method for the enzymatic transfer of sugar molecules to an optor, useful for synthesis of e.g. polysaccharide bioadhesives delivery systems, including hybrid molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 CCATTIGAAGTCGTIGTIGCAGATGATGGTAGTAAGGAAAACTTACTTACCATTGTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           661 AAATACGAACAAAAACTTGACATAAAGTATGTAAGACAAAAAGATTATGGATATCAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                      TGCGATAGCTCATTAGATATCGCAACACAGCTCTTACTTTCCAACGTAAAAAATTAACT
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                                                                                                                                                                                                                                                                                                      2979;
                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                              Length
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0
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                                                                                                                                                                                                                                        Sequence 2979 BP; 1129 A; 466 C; 497 G; 887
                                                                                                                                                                                                                                                           100.0%; Score 2979;
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                              Claim 16; Page 86; 86pp; English
                                                                                                                                                                                                                     injuries or surgical sites.
                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 2979; Conservative
                   WPI; 2000-376319/32.
P-PSDB; AAY96213.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     multocida chondroitin synthase. A chondroitin polysaccharide may be used as a hyaluronan polysaccharide substitute in medial or cosmetic applications, for example in eye or joint applications, for moisturiser or wound dressings. The enzyme may be used in covalently coupling specific drugs, proteins or toxins to the structurally modified procedures, covalently cross linking the hyaluronic acid itself or to other supports to achieve a gel or other three dimensional biomaterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the coding sequence of the Pasteurella
                                                                                                                                                                                                                                                                                                 Chondroitin synthase; dermatan sulphate; chondroitin sulphate polymer; eye application; joint application; moisturiser; drug delivery; wound dressing; biocompatible film; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New chondroitin synthase gene obtained from Pasteurella multocida, useful as hyaluronan polysaccharide substitute in medial or cosmetic applications, e.g. for eye or joint applications, for moisturizer or wound dressings
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QQ	1201	GGAATGGCCATCCATCAAGAACCACCTGGTAAAGAAAATGAAACAGAACG	Ğ.
QY Dp	1261	GCTGGTAAAAGTATTACGCTTAAAÁTTGTGAAAAGAAAGGTACCTTACATCTAGAAAG 	1320
δy da	1321	CTTTTACCAATAGAAGATTCACATATTCATAGAATACCTTTAGTTTCTATTATATACCCC	1380
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QY Db	1741	GCTAATGGTTACAATTGGCCAGAATTTTCACGAGAAAAACTCACAACGGCTATGATTGCT 	0 0
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QY	1861	ATTGAAAACGCCG7 ATTGAAAACGCCG7	1920
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The present invention relates to the coding sequence of the Pasteurella multocida chondroitin synthase. A chondroitin polysaccharide may be used as a hyaluconan polysaccharide substitute in medial or cosmetic applications, for example in eye or joint applications, for moisturiser or wound dressings. The enzyme may be used in covalently coupling specific drugs, proteins or toxins to the structurally modified chondroitin for general or targeted drug delivery or radiological procedures, covalently cross linking the hyaluronic acid itself or to other supports to achieve a gel or other three dimensional biomaterial with stronger physical properties, and covalently linking hyaluronic acid to a surface to create a biocompatible film or monolayer. The present sequence is one version of the coding sequence of the invention.
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Matches 2969; Conservative
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                                                                                               This DNA sequence codes for the hyaluronate synthase (pmHAS, see AAY06212) of Pasteurella multocida Carter Type A. The pmHAS enzym has different kinetic optime with respect to pH and metal ion dependence, and different Km values compared with the HAS enzymes of Streptococcus equisimilis (see AAY06206) and Streptococcus of Straptococcus and always are about 2 - to 3 -fold lower for IOPs sugars, and Vmax values are about 2 - to 3 -fold higher. The invention provides recombinant vectors containing hyaluronate synthase DNA,
        AATGAACAAATTCAAAGTGCAAAAAAGGCGAAAATATCCCCGTTAACAAGTTCATTATT
ATGAATGTGAAAGGGGCATCACAAGGTATGTTTATGAAGTATGCGCTACCGCATGAGCTT
                                AACACTGAGGATATTTGGTTCCAATTTGCACTTTTAATCTTAGAAAAGAAAACCGGCCAT
                                                                                                                                                 AATGAACAAATTCAAAGTGCAAAAAAAGGCGAAAATATCCCCGTTAACAAGTTCATTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , hyaluronate synthase for production of controlled molecular weight and targeting
                                                                                                                                                                                                                                                                                             synthase; pmHAS; hyaluronic acid; hyaluronan;
                                                                                                                                                                                                                                                                            multocida hyaluronate synthase pmHAS DNA
                                                                                                                                                                          2941 AATAGTATAAAGGCTATAAAAACATTTGCATTTTATTAAAA 2979
                                                                                                                                                                  AATAGTATAACGCTATAAAACATTTGCATTTTATAAAA 2979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 123-125; 125pp; English
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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especially S. equisimilis hyaluronate synthase DNA (see AAX58841), and prokaryotic or eukaryotic host cells which produce the enzyme and its hyaluronic acid product, particularly a product with modified structure or molecular size. The hyaluronic acid produced this way is purer than that produced by conventional methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 ATTTTTAAAGGAAAGAAATGAATACATTATCACAAGCAATAAAAGCATATAACAGCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGATGGTAGTAAGGAAAACTTACTTACCATTGTGCAAAAATACGAACAAAAACTTGAC
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                                                                                                                                                           DB 20; Length 2937
                                                                                                                     Sequence 2937 BP; 1077 A; 482 C; 509 G; 869 T; 0 other;
                                                                                                                                                           Score 2283.4;
                                                                                                                                                                                 Pred. No. 0;
0; Mismatches
                                                                                                                                                             76.6%;
86.5%;
                                                                                                                                                                               Best Local Similarity 86.5
Matches 2540; Conservative
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982	AATATATCGTTGGATTGGAGATTAGAACATTTCAAAAAACCGATAATCTACGTCTATGT 1041
1042	GATTCTCCGTTTCGTTATTTTGTTGCGGGTAATGTTGCATTTTCTAAAGAATGGCTAAAT 1101
1102	AAAGTAGGTTGGTTCGATGAAGAATTTAATCATTGGGGGGGCGAAGATGTAGAATTTGGT 1161
1162	TACAGATTATT TATCGCTTATT
1222	
1282	AAAATTGTGAAAGAAAGGTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCA 1341
1342	CATATTCATAGAATACCTTTAGTTTCTATTATATCCCGCTTATAACTGTGCAAATTAT 1401
1402	2 ATTCAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATT 1461
1462	2 TGTAACGATGGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAAT 1521
1523	2 CCTAGGGTACGCATCATGTCTAAACCCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCC 1581
1587	2 GTTTCTTTTGCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCT 1641
1642	2 GATGCAGTTGAACTGTGTTTAAAAGAATTTTTAAAAGATAAAACGCTAGCTTGTGTTTAT 1701
1702	
176.	2 GAATTTTCACGAGAAAAACTCACAACGGCTATGATTGATGCTCACCATTTTAGAATGTTTACG 1821
182	2 ATTAGAGCTTGGCATTTAACGGATGGATTTAACGAAAATATTGAAAACGCCGTGGATTAT 1881
188	2 GACATGTTCCTTAAACTCAGTGAAGTTGGAAAATTTAAACATCTTAATAAAATCTGCTAT 1941
194	2 AACCGCGTATTACATGGTGATAACACATCCATTAAGAAACTCGGCATTCAAAAGAAAAAG 2001
200	2 CATTITCTTGTAGTCAATCAGTCATTAAATAGACAAGGCATCAATTATTATAATTATGAC 2061

2541 2241 2460 2520 2181 2160 2361 2340 2400 2481 2301 2421 ATCACATCCTGCCAATTGATAGTGTGCCAGAATATAACACTGAGGATATTTGGTTC 2781 CATITIGITGIAGICAAICAGICATIAAAIAGACAAGGCAIAACITAITAIAAITAIGAC 2040 2281 GATATCAAAAAAGAAATACTAGCCTTCTATCATAAACATCAAGTGAATATTTACTAAT 2161 GTCAGTATTTTTTTATCCCAATACATTAAACGGCTTAGTGAAAAAACTAAACAATATTTT GAATATAATAAAAATATATTCGTTATTATTCTACATGTTGATAAGAATCATCTTACACCA 2221 GAATATAATAAATATATTGGTTATTGTTCTACATGTTGATAAGAATCATCTTACACCA 2302 GACATCAAAAAAGAAATATTGGCTTTCTATCATAAGCACCAAGTGAATATTTTACTAAAT GTCAGTATTTTCTATCCCAATACATTAAACGGCTTAGTGAAAAAAACTAAACAATATTATT multocida hyaluronate synthase (PmHAS) nucleotide sequence BP 2937 (first entry) AAZ35589 standard; DNA; 01-FEB-2000 AAZ35589; 2761 2902 2581 2722 2701 2782 2842 2821 2881 2602 1981 2062 2041 2122 2101 2182 2242 RESULT 5 AAZ35589 X E X E X S X E X g g g Dp g ò δy δ q qq q δy qq δ q δ g δy QQ Óλ g QΥ ð g QΥ δ g Ω ò δ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be used in e.g. drug delivery, angiogenesis and wound healing, stabilisation of recombinant proteins and in cosmetics. The HS nucleic acids can also be used to develop agents to block capsule synthesis by pathogens and act as antiblotics. The avirulent P. multocida strains can
                 cosmetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated hyaluronate synthase nucleic acids, used for the production of hyaluronic acid, for developing antibiotics and vaccines
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uronate synthase; PmHAS; hyaluronan; hyaluronic acid; HA;
dellvery; anglogenesis; wound healing; capsule synthesis;
cholera; shipping fever; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2283.4; DB 21; Length
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 376; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used as vaccines for fowl cholera or shipping fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 113-114; 121pp; English.
                                                                                                                                                                                                                                                                "Hyaluronate
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and for diagnostic applications
                                                                                                                                                                                                                                       PMHAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.6%;
86.5%;
                 Hyaluronate synthase; PmHAS;
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                                                                                                                Pasturella multocida
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cataract; arthritis; ulcer;
hyaluronic acid production;
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99US-0283402.
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P-PSDB; AAY96212.
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The present sequence is the coding sequence of the soluble recombinant form of Pasteurella multocida hyaluronic acid synthase-D, PmHAS-D. This sequence encodes residues it or 703 of the 972 residues of the native FMHAS enzyme. PmHAS-D catalyses glycosaminoglycan polymerisation to produce hyaluronic acid, HA: a linear polysaccharide. HA has viscoelastic produce hyaluronic acid, HA: a linear polysaccharide. HA has viscoelastic consecutation which makes it useful for a number of applications. HA can be used during ophthalmic surgery as a viscoelastic replacement for the vitreous humour e.g. during implantation of intraocular lenses in cataract patients. HA injections directly into joints is also used to alleviate pain associated with arthritis. HA can also be used as bioadhesives for haemostatic sealing and healing of wounds and surgical incisions; and as biomaterials that provide custained delivery of encapsulated drugs, to wounds, ulcers, injuries or surgical sites. The present sequence can therefore be used to produce HA. or bioadhesives polysaccharide drug delivery systems, including hybrid molecules ø. oţ 86pp; English synthesis acceptor, useful for Page 84; 20; Claim

Sequence 2112 BP; 745 A; 359 C; 387 G; 621 T; 0 other;

ï 399 459 219 279 240 339 519 480 579 639 669 300 360 420 481 TCTATTATCGTTACAACATTCAATCGACCAGCAATTTTATCGATTACATTAGCCTGTTTA 540 AAAGATTATGGATATCAATTGTGTGCAGTCAGAAACTTAGGTTTACGTACAGCAAAGTAT 759 AAATTATTTGAGAAGTCTGCTGAAACCTACGGGCGAAAAATCGTTGAATTCCAAATTATC 180 AAATTATTTGAAAAGTCGGCGGAAATCTATGGACGGAAAATTGTTGAATTTCAAATTACC 120 AAATGCCAAGAAAAACTCTCAGCACATCCTTCTGTTAATTCAGCACATCTTTCTGTAAAT 180 Gaps **AAATCTATCACTGGGAAAAAA**TCGGAGAACGCAGAAATCAGAAAGGTGGAACTAGTACCC AAAGATTTTCCTAAAGATCTTGTTCTTGCTCCATTGCCAGATCATGTTAATGATTTTACA TGGTACAAAAATCGAAAAAAGCTTAGGTATAAAGCCTGTAAATAAGAATATCGGTCTT AAATGTAAAGAAAAACTCTCGACCAATTC--------TTATGTAAGT GAAGATAAAAAAAACAGTGTTTGCGATAGCTCATTAGATATCGCAACACACCGCTCTTACTT AAAGATTTTCCCAAAGATCTGGTTTTAGCGCCTTTACCTGATCATGTTAATGATTTTACA TCTATTATTATTCCTACATTTAATCGTAGCCGTATTTTAGATATAACGTTAGCCTGTTTG GTCAATCAGAAAACAAACTACCCATTTGAAGTCGTTGTTGCAGATGATGGTAGTAAGGAA AACTTACTTACCATTGTGCAAAAATACGAACAAAAACTTGACATAAAGTATGTAAGACAA DB 21; Length 2112; 21; 50.5%; Score 1503.2; DB 21; Lengt llarity 82.5%; Pred. No. 2.8e-281; Conservative 0; Mismatches 348; Indels _ = = = -= = = Similarity Best Local Sim Matches 1743; Query Match 121 19 220 280 421 580 541 640 61 181 121 340 301 400 361 460 520 501 200 g qq g ò q g ð g ò ò ò δ ò g ò 셤 ç q δý g ò g ò

1119 1179 1200 1299 1260 1320 1500 1599 1659 1620 1719 1680 1059 960 GAAGAATTTAATCATTGGGGGGGGGGAAGATGTAGAATTTGGTTACAGATTATTGCCAAA GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGCATCATG AATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTGGCCAGAATTTTCACGAGAAAAA AAAGATAACGGTTTTCAAGCCAGTGCCGCTCGGAATATGGGATTACGCTTAGCAAAATAT ACACAACATATTGACCCCAAAAGACTTCTTAAATAACGCGAGTTTGCTTGAATCATTACCA AGATTAGAACATTCAAAAAACCGATAATCTACGTCTATGTGATTCTCCGTTTCGTTAT GTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTCGCATATCAATAGAGTACCT TTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGTGTAGAT AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA TCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTTGCTAAAGGT AATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTGGCCAGAATTTTCACGAGAAAAA AATCCGGATGGTTAATTGGTTACAATTGGCCAGAATTTTCACGAGAAAAA GATTTTGTCTCGATTCTAGACTGCGATATGGCACCACAACTTATGGGTTCATTAT GTTGCAGAGCTATTAGAAGATGATGATTTAACAATCATTGGTCCAAGAAAATACATCGAT **ACTCATAATATTACCGCAGAACAATTCCTTAACGATCCATATTTAATAGAATCACTACCT** GAAACCGCTACAAATAACAATCCTTCGATTACATCAAAAGGAAATATATCGTTGGATTGG GTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCACATATTCATAGAATACCT TATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGAACTGTGT CTCACAACGGCTATGATTGCTCACCATTTTAGAATGTTTACGATTAGAGCTTGGCATTTA 1000 1321 1441 1540 781 841 1060 1021 1120 1081 1180 1141 1240 1201 1300 1261 1360 1420 1381 1480 1600 1561 1660 1621 1720 1681 721 320 380 940 901 1501 091 961 g g q g g q 셤 g g g g g à ò ò ò ò qq ò g g g ò g q QΥ ò ò ò οý ò ò ò ò ò δ

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                                                                                                                                                                                                                                         1980
                                                                                                                                                                                                                                                                                                                                                                          ACGGATGGAHTTAACGAAAATATTGAAAACGCCGTGGATTATGACATGTTCCTTAAACTC 1899
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                                                                                                                                                                                                                         GATAACACCATTAAGAAACTCGGCATTCAAAAGAAAAACCATTTTGTTGTAGTCAAT
                                                                                                                                                                                                                                                                                        CAGTCATTAAATAGACAAGGCATCAATTATTATTATTATGACAAATTTGATGATTTAGAT
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                                                                                                             AGTGAAGTTGGAAAATTTAAAACATCTTAATAAAATCTGCTATAACCGCGTATTACATGGT
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97US-0044031.
97US-0046655.
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06-MAY-1997;
16-MAY-1997;
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                                                                                                                                                                                                                                                                                     1354 ATACCTTTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGT 1413
                                                                                                                                                                                                                                                                                                                                  1001 ATGCCCAAAATTAGTATTATTGTTCCTGTATACAATGTAGAAAAATATTAGAAAAATGT 1060
                                                                                                                                                                                                                                                                                                                                                                                     GTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGT 1473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTTGCT
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                                                                                                                                         Sequence 5550 BP; 1940 A; 806 C; 1041 G; 1763 T; 0 other;
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                                                                                                                                                                                         Score 86; DB 20;
Pred. No. 2.3e-07;
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ilarity 54.0%;
Conservative
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AAZ45258:
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The present invention relates to nucleic acid sequences (ABG6/188-ABG71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines.
                                                                                                                                                                                                                                  ACCTTTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGT 1415
                                                                                                                                                                                                                                                                                  1416 AGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTC 1475
                                                                                                                                                                                                                                                                                                                                 AACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGCAT 1535
                                                                                                                                                                                                                                                                                                                                                                                 CATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTTGCTAA 1595
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                                                                                                                                                                                                                                                                                                 126 GACTGATAATTCAGCTAAAGTCATAAAAGTATCTCAGATAA-----TCGAATTCGTTA 179
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                                                                                                                        of the printed specification, but was obtained in electronic fo directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                    Length 984;
                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electron
                                                                                                                                                                               2.7%; Score 81; DB 24; Length 98
55.4%; Pred. No. 1.7e-06;
ive 0; Mismatches 140; Indels
                                                                                                                                                          Sequence 984 BP; 360 A; 136 C; 190 G; 298 T; 0 other;
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Note: The sequence data for this patent did not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1356 ACCTTTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTG 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1416 AGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTC 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1476 AACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGCAT 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1536 CATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTTGCTAA 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1596 AGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGAACT 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 GACTGATAATTCAGCTAAAGTCATAAAAGTATCTCAGATAA-----TCGAATTCGTTA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 TTTTGAAAAAGAAAATGGCGGACAAGCTACTGCCCGAAATTTTGGATTAGATGTGGCTAC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 GGGAGATTACATCGTGATGGTAGATAGTGATGATTACATTAGCAAAAACCTAGTAGAAAC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 ACCTITAGTAAGTGTAATTATTCCAGTTTATAATGTAGAAAAGTATGTTAAACGATGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection,
treatment and prevention of infection, also related polypeptides, antibodies and modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding enzymes involved in exopolysaccharide biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the printed specification, but was obtained in electronic for directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 984 BP; 360 A; 136 C; 190 G; 298 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.7%; Score 81; DB 24;
55.4%; Pred. No. 1.7e-06;
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                                                                                                                                                                                           Claim 16; SEQ ID 2768; 180pp; French.
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/*tag= a
/product= "EPS1"
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The present sequence encodes enzymes involved in the biosynthesis of exopolysaccharides (EPS). These enzymes are designated EPS1-EPS10, and are encoded by open reading frames eps1-eps10. The enzymes are isolated from Streptococcous thermophilus strain Sfi39. The proteins are used in a method for the synthesis of EPS, which includes at least one step of forming a bond (alpha or beta-isomer) between C-1 (carrying the reducing aldehyde function, of an activated D-galactose pyranose), and a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis of EPS occurs with, in each step, addition of a new sugar unit, through its hemi-acetyl function, to an alcoholic hydroxyl of a second sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-SSDB; AAYS4065, AAX54066, AAX54067, AAX54068, AAY54069, AAX54070.
AAX54071; AAX54072, AAX54073, AAX54074.
                                                                                                                                                                                                                            /note= "encodes AAY54070; contains 1 stop codon at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properties fermented milk products
                                                                                                                                                                                                                                                                                                                                                                    /product= "EPS9"
/note= "encodes AAY54073"
16919..18016
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12838..13788
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14138..15553
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                                                                                                                                                                                  rnote= "encodes AAY54069"
1633..10681
                                                                                                                                     /note= "encodes AAY54068'
5629..6996
"encodes AAY54065'
                                           == "encodes AAY54066"
..4822
                                                                                        "encodes AAY54067
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/product= "EPS10"
                                                                                                                                                                                                                                                                                                                         'product= "EPS8"
                                                                                                                         product= "EPS4"
                                                                                                                                                                                                                                                                              "EPS7"
                                                                             'product= "EPS3"
                                                                                                                                                                        "EPS5"
                                                                                                                                                                                                                     'product= "EPS6"
                                 product- "EPS2"
                                                                                                                                                                                                                                                        10703..11671
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98EP-0201312.
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22-APR-1998;
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unit, present at the end of a chain of sugar residues bonded to the primer. EPS1 to EPS4 are used to elongate the EPS chain, and to regulate EPS production, EPS5 is used in the blosynthesis of EPS7 and EPS8 are beta-glycosyltransferases. EPS9 is a transporter of repetitive units, and EPS10 catalyses the conversion of a pyranose form of a beta-joalactose to the furanose form. The EPS enzyme are used to improve properties of foods, particularly fermented milk products such as yoghurt and cheese,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12974 CGCTACCAGTAATTTCCGATTTAATCTGTAGTCATCATAATATTAAGGTAATCAACCAAA 13033
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                                                                                                                                                                                                                                                                                                                                                                                                           1427 TIAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACAGATAATA 1486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of the eps operon of S. thermophilus Sfi39.
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                                                                                                                                                                                                     2.7%; Score 80; DB 21; Length 19966; 52.0%; Pred. No. 4.1e-06;
                                                                                                                                                                      Sequence 19966 BP; 6405 A; 3134 C; 3732 G; 6694 T; 1 other;
                                                                                                                                     e.g. their organoleptic properties and flavour stability.
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                                                                                                                                                                                                                                          0; Mismatches 165;
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2703...3389
/*tag= a
/product= "eps1"
/note= "encodes AAY43767"
3390...4121
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/note= "encodes AAY43769"
4832..5530
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                                                                                                                                                                                                           Query Match 2.77
Best Local Similarity 52.0
Matches 179; Conservative
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12914 TAGCTCAAACATATCGCAATATTGAAGTCATTATAGTAAATGATGGTAGCACAGATCAGT 12973
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                                                                                                                                                                                                         12794 ACTGTTAGAATATGATTTTATATTAGAGTAGAATAAAGAGATGAATGCATTAATAT 12853
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                                                                                                                                                                                                                                              1367 CTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGTAGATAGTGCTC 1426
a free-flowing character and/or a smooth, creamy texture to acidified milk products (yoghurt or cheese).
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Beta-1,3-galactosyltransferase; alpha-2,3-sialyltransferase;
sialic acid synthase; CMP-sialic acid synthetase; mimic; antibody;
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                                                                                              Length 19966;
                                                         T; 1 other;
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/note= "Open reading frame 6a"
                                                                                                                Pred. No. 4.1e-06;
0; Mismatches 165; Indels
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/note= "Open reading frame 5a"
                                                         Sequence 19966 BP; 6405 A; 3133 C; 3732 G; 6695
                                                                                            DB 21;
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o frame 3a"
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1234..2490
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                                                                                            Score 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunity; immunogen; ganglioside; ds
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                                                                                            2.78;
52.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPS core biosynthesis locus.
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                                                                                                                Best Local Similarity 52.0
Matches 179; Conservative
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                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the eps operon of Streptococcus thermophilus Sf193. The operon contains 10 open reading frames, and encodes enzymes (eps1, eps2, eps3, eps5, eps6, eps7, eps8, eps9 and eps10) that are involved in the biosynthesis of exopolysaccharides (EPS). The enzymes catalyse the formation of specific intersugar bonds. The enzymes catalyse a process that includes at least one step of forming a bond (in alpha or beta anomeric form) between Cl, carrying the reducing aldehyde group of an activated D-Galp (galactose in pyranose form), and a phosphate group on a lipophilic or proteinaceous primer. The enzymes are used to produce Eps that have antitumor or problotic properties or are used in foodstuffs to improve organoleptic qualities and flavour. When expressed by lactic acid bacteria, EPS impart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'encodes AAY43776; this CDS, minus the
termination codon, is specifically claimed
(claim 6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant enzymes for biosynthesis of exopolysaccharides having e.g. antitumor or probiotic properties or useful in fermented milk products
                                                                                                                                                                 /product = "eps6; this CDS, minus the termination codon, is specifically claimed (claim 6)" /note= "encodes AAY43772; contains a stop codon at nucleotides 9410-9412"
                                                                                                                                                                                                                                                                                                                                                                                        /note= "encodes AAY43774; this CDS, minus the termination codon, is specifically claimed (Claim 6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY43770, AAY43771, AAX43772,
                                                                                                                                                                                                                                                                                               /hote= "encodes AAY43773; this CDS, minus the termination codon, is specifically claimed 12838..13788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "encodes AAY43775; this CDS is specifically claimed (claim 6)"
                                                                                                            note= "encodes AAY43771"
633..10681
                                       "encodes AAY43770"
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P-PSDB; AAY43767, AAY43768, AAY43769, AAY43776.
AAY43773, AAX43774, AAX43775, AAX43776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "eps10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "eps9"
                 "eps4"
                                                                                            "eps5"
                                                                                                                                                                                                                                                                                   "eps7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98EP-0201310.
98EP-0201311.
98EP-0201312.
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                                       'note= "enc
629..6996
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us-09-842-484a-1.rng

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s a reaction mixture for the synthesis of a sialylated oligosaccharide is useful for synthesising sialylated oligosaccharide such as ganglioside, lysoganglioside or their mimings. Glycosyltransferases are useful for chemo-enzymatic Synthesis of oligosaccharides, including gangliosides and other oligosaccharides that have biological activity. The enzymes and nucleic acids that encode them cler useful for studies of the pathogenesis mechanisms of organisms that synthesize ganglioside mimics, such as C. jejuni and the nucleic acids are used as probes to study expression of genes involved in ganglioside mimetic synthesis. Antibodies raised against the glycosyltransferases are also useful for analyzing the expression patterns of these genes involved in pathogenesis. The oligonucleotides for inhibiting expression of the Campylobacter cards are also useful for designing antisense oligonucleotides for inhibiting expression of the Campylobacter cargmes that are involved in the biosynthesis of ganglioside mimics cargmes that are involved in the biosynthesis of ganglioside mimics of immunocers for expression are useful as diagnosing reagents or as therapeutics of an assimunocers for expendict and are involved in the biosynthesis or as therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and as immunogens for producing antibodies. Bacterial glycosyltransferase can be used to catalyse the formation of oligosaccharides that are identical to the corresponding mammalian structures and are easier and less expensive to produce in large quantity. Compared to the mammalian glycosyltransferase. The bacterial origin of the enzymes facilitates expression of large quantities of the enzymes using relatively inexpensive prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY97200, AAY97201, AAY97202, AAY97203, AAY97204, AAY97205
AAY97206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel glycosyltransferase polypeptides and polynucleotides useful biosynthesis of ganglioside and ganglioside mimics, as diagnostic reagents and as immunogen for producing antibodies
                                                                                                                                                                                                                                                                                                                                                /product Lipooligosaccharide biosynthetic enzyme/note "Open reading frame 12a"
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                                                                                                                                                                                            /product= Sialic acid biosynthetic enzyme
                                                                                                                                                                                                                                                                         'product= CMP-sialic acid synthetase
                    ....ucue CstII sialyltransferase
/note= "Open reading frame 7a"
6924..7964
                                                                                                                                                                                                                                                                                         /note= "Open reading frame 10a"
complement (10554..11366)
                                                                                                                 'product Sialic acid synthase
                                                                                                                                                                                                                  "Open reading frame 9a"
                                                                                                                                     "Open reading frame 8a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 86-90; 120pp; English.
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31-JAN-2000; 2000US-0495406.
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5048..6923
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for

DB 21; Length 11474;

2.7%; Score 79.2;

Query Match

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                                                                          11424 AAATTTCCTAAACTTTGATAGAATTGTTTTTATTTTTAACAAAATTTAGGAAAATAT 11365
                                                                                                                                                                                                                                       1476 AACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGCAT 1535
                                                                                                                                                                                                                                                                                                   CAT --- GICTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTGC 1592
                                                                                                         1356 ACCITIAGITICIAITIAIATACCCCGCTIATAACTGTGCAAATTATATTCAAAGATGTGT 1415
                                                                                                                                                                        1416 AGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTC 1475
                                            1296 AAAGGTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCACATATTCATAGAAT 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer: eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                1593 TAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTGTGTTTAAAAGAATTTTTAAAAGATAAAACGCTAGCTTGTGTTTATACC 1704
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                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune system associated gene SEQ ID NO: 2331.
pred. No. 5.4e-06;
0; Mismatches 198;
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01-SEP-2000; 2000DE-1043826
    51.2%;
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                  211; Conservative
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   Best Local Similarity
Matches 211; Conserv
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                     present invention provides a number of human immune system associated
                                   genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
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                                                                                         macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilopsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                       6941 АААТААААААААААААААААТАААТАААТСААСАААТАААТАААТАААТАААТАААТТААТТ 6882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.6%; Score 77.2; DB 24; Length 12237;
47.8%; Pred. No. 1.3e-05;
tve 0; Mismatches 278; Indels 1;
                                                                                                                                                                                   Sequence 12237 BP; 3050 A; 207 C; 3024 G; 5956 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune system associated gene SEQ ID NO: 1405.
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                                                                                                                                                                                                                                          Similarity
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Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.6%; Score 77.2; DB 24; Length 17527; 43.9%; Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17527 BP; 4501 A; 296 C; 4094 G; 8636 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1405; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 543;
                                                                                                                                                                                                                  χ,
                                                                                                                                                                                                                  Berlin
                                                                                                                       2000DE-1032529
2000DE-1043826
                                                                                   02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 434; Conservative
                                                                                                                                                                                                                  Piepenbrock C,
                                                                                                                                                                              (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                    WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                 WO200200928-A2
                                                                                                                         30-JUN-2000;
                                                                                                                                          01-SEP-2000;
                                                   03-JAN-2002
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16107 TATCCCTATTAAAAATCAAAACTATCTCTCATATATTCCTTCAAACATAACTATAAATTA 16048
                     16467 TACGACCAAACTAACCAAAATAACGAAATCCCGTCTCTACTAAAAAACACACAAAAAAA 16408
                                                                                          2832 BACATCGACCTGACTTATATGCCTTGGGAACGAAAATTACAATGGACAAATGAACAAAT 2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, cytostatic; anti-tumour; metabolism; metabolic disease; liver;
solid tumour: cancer; cytosine methylation; epigenetic; eye, kidney;
single nucleotide polymorphism detection; SNP; stool; urine; lung;
cerebral-spinal fluid; intestine; brain; heart; prostate;
DUSP2; EPHX2; QDPR; SGSH; SHMT2; SLC7A2; SLC7A4; TYMS; ds.
2532 CGGCATGAATTTCTCAGCATTAACACATGATTGGATCGAGAAAATCAATGCGCATCCACC 2591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid, useful for diagnosis and therapy of metabolic disease, solid tumour and cancers, comprises segment of chemically modified genomic sequences of genes associated with metabolism - \,
                                                                                                                                                                                                                                                 TATTTGGTTCCAATTTGCACTTTTAATCTTAGAAAAGAAAACCGGCCATGTATTTAATAA
                                                                                                                                                      16347 TACTTAAACCCAAAAAATAAAATTACTATAAACCTAAAATCCTACCATTACACTCCAACC
                                                                                                                                                                                                                                                                              2892 TCAAAGTGCAAAAAAAGGCGAAAATATCCCCGTTAACAAGTTCATTAATAATAACA
                                                               ATTTAAAAAGCTGATTAAAACCTATTTTAATGACAATGACTTAAGAAGTATGAATGTGAA
                                                                                                                           AGGGGCATCACAAGGTATGTTATGAAGTATGCGCTACCGCATGAGCTTCTGACGATTAT
                                                                                                                                                                                     TAAAGAAGTCATCACATCCTGCCAATCAATTGATAGTGTGCCAGAATATAAACACTGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemically pretreated metabolism associated gene #27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16047 CAAAATATTATCCCCAATTTTATAACA 16020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 79-84; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS63332 standard; DNA; 17527 BP
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG.
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07-APR-2000;
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The invention relates to a nucleic acid (I) comprising a sequence at associated with metabolism such as DUSP2 (NM_00418), EPHXZ (NM_001979), associated with metabolism such as DUSP2 (NM_00412), EPHXZ (NM_001979), copp. (NM_000320), SGSH (NM_00199), SIHMZ (NM_001071), SIC7A2 (NM_003046), SLC7A4 (NM_00173) and TYMS (NM_001071) (all tabolism subsidiation of DNA sequences, for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNS) in a chemically created DNA of genes associated with metabolism. An array of (I) is treated DNA of genetic and/or epigenetic parameters for the application of DNA sequences, for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNS) in a chemically consistent of analysing cytosine methylations. The method involves chemically treating genetic and/or epigenetic parameters for the specific diseases by analysing cytosine methylations. The method involves chemically treating genomic DNA ample by a solution of bisulphite, chemically treating genomic DNA ample by a solution of bisulphite, which is dissimilar to cytosine in terms of hybridisation behaviour and amplifying fragments of the chemically pretrated genomic DNA. The genomic DNA is from cells or cellular components which contain DNA, cources of DNA comprising, for e.g. cell lines, biopsies, blood, sputum, created restrictions, detections, prostate, lung, breast contained or metabolism and sequences further required for their regulation. Contained to their regulation. Metabolism and sequences further required for their regulation. Contained to metabolism associated with a caretal modifications of genes associated with a caretal modifications of genes associated with a caretal parameters are in particular cytosine methylations of histones which correlated metabolism second metabolism second metabolism characterial metabolism characterial metabolism characterial metabolism second metabolism second metabolism second metabolism characterial parameters are in particular sincled metab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16876 AAAATITAAAATAACAATAAACCAAAATCACACCACTATACTCCCAACCTAAACAAAA 16817
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Pred. No. 1.4e-05;
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                        US-09-842-484A-1
2979
                                                                                                                        January
                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                           Scoring table:
                                                                               OM nucleic
                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                        Run on:
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Issued_Patents_NA:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli	7	7	'n	186	Sequence 288, App	Sequence 1137, Ap	Sequence 71, Appl	Н	13	86,	199,	Sequence 595, App	Sequence 1, Appli	19	14, 7	121	Sequence 2, Appli	Sequence 191, App	-	H	534	Sequence 1, Appli	683	Sequence 786, App	Patent No. 5231168	Sequence 11, Appl
SUMMARIES	ID	US-09-437-277-4	US-09-437-277-2	US-08-597-236-1	US-08-746-682A-1	US-08-998-416-186	US-08-998-416-288	US-08-998-416-1137	US-08-961-527-71	US-08-559-896B-1	US-08-487-826B-13	US-08-961-527-86	US-08-961-083-199	US-08-998-416-595	US-09-056-075-1	US-08-961-083-197	US-08-232-463-14	US-09-453-702B-121	US-07-867-106-2	US-08-998-416-191	US-08-446-855A-1	US-09-150-741-1	US-08-998-416-534	US-09-426-290-1	US-08-998-416-683	US-08-998-416-786	5231168-1	US-08-920-812-11
	DB	4	4	Н	Н	4	4	4	4	4	7	4	٣	4	7	٣	-	4	~	4	7	4	4	4	4	4	9	7
	o Query Match Length DB	2979	2112	14602	14602	615	837	636	32768	1956	19124	19390	2023	658	6243	811	7218	14187	5852	663	8920	8920	854	168575	724	711	3095	3480
d	Query Match	100.0	50.5	2.5	2.5	2.5	2.4	2.4	2.3	2.5	2.1	2.0	2.0	2.0	1.9	1.9	1.9	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.7	1.7	1.7	1.7
	Score	2979	1503.2	74.6	74.6	74.2	9.07	70.2	67.2	9.99	63.2	61	9.09	58.8	57.8	57.6	55.6	52	54.2	53.8	53.6	53.6	52.2	52.2	51.6	51	51	51
	Result No.		7	e	4	υ v	و د	c 7	8	6	10	c 11	12	c 13	c 14	15	c 16	c 17	c 18	19	20	21	22	c 23	c 24	c 52	36	27

Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 13, Appl Sequence 2, Appl Sequence 2, Appl Sequence 10, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 8, Ap	Sequence 3, Appli
US-08-920-827-11 US-08-921-177-11 US-08-920-177-11 US-08-920-828-11 US-08-119-704-5 US-08-119-704-5 US-08-119-704-5 US-08-119-704-10 US-08-109-116-083-2 US-08-107-755A-32 US-08-107-755A-32 US-08-107-755A-8 US-08-107-755A-8 US-08-107-755A-8 US-08-107-755A-8 US-08-107-755A-8 US-08-107-755A-8 US-08-107-755A-8 US-08-107-755A-8 US-08-107-755A-8 US-08-107-755A-8 US-08-107-755A-8 US-08-107-755A-8 US-08-107-755A-8 US-08-107-755A-8	US-08-568-459A-3
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C C C 3310 28 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	45
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RESULT 1
US-09-437-277-4
; Sequence 4, Application US/09437277
; Patent No. 6444447
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
; TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
; FILE REFERENCE: 5820.551
; CURRENT APPLICATION NUMBER: US/09/437,277
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: WordPerfect 8.0 (saved in ASCII format)
; SEQ ID NO 4
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-09-437-277-4

ALIGNMENTS

Gaps ö Length 2979; Indels ; ; DB 4; Query Match 100.0%; Score 2979; Best Local Similarity 100.0%; Pred. No. 0; Matches 2979; Conservative 0; Mismatches

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240 61 ATGAATACATTATCACAAGCAATAAAAGCATATAACAGCAATGACTATGAATTAGCACTC 120 240 300 420 ATGAATACATTATCACAAGCAATAAAAGCATATAACAGCAATGACTATGAATTAGCACTC 120 121 AAATTATTTGAGAAGTCTGCTGAAACCTACGGGCGAAAAATCGTTGAATTCCAAATTATC 180 TGCGATAGCTCATTAGATATCGCAACACACTCTTACTTTCCAACGTAAAAAATTAACT 300 9 9 61 361 241 301 301 q qq ò ò δ g ò q οχ g ŏ g ò g

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us-09-842-484a-1.rni

CGAAAAAA 480 CGAAAAAA 480	TACATTT 540 TACATTT 540	AAACTAC 600 AAACTAC 600	TGCAA 660 GCAA 660	AATTG 720 AATTG 720	TAGAC 780 TAGAC 780	GAAGAC 840 GAAGAC 840	CAGAA 900 CAGAA 900	AACAAT 960 AACAAT 960	CAAAAAA 1020 CAAAAAA 1020	GTTGCA 1080 GTTGCA 1080	GGGGG 1140 GGGGG 1140		SGCGAA 1260 GCGAA 1260	AGAAAG 1320 	ATCCCC 1380 ATCCCC 1380	ACTGTT 1440 ACTGTT 1440	STGATC 1500 STGATC 1500	CGGAATA 1560
STTAATGATTTTACATGGTACAAAAATGGAA 	AATATCGGTCTTTCTATTATTATTCCC 	agcctgtttggtcaatcagaaaac 	GATGGTAGTAAGGAAAACTTACTTACCATTG 	IGACATAAAGTATGTAAGACAAAAAGATTATGGATATC: 	CGTACAGCAAAGTATGATTTTGTCTCGATTCT 	GGGTTCATTCTTATCTTACAGAACTATTA 	SGACCTAGAAAATATGTGGATACTCATAATATTACCGC 	TTAATAGAATCACTACCTGAAACGGCTACAATE 	3GATTGGAGATTAGAACATTT 	TCTCCGTTCGTTATTTGTTGCGGGTAATG	GTAGGTTGGTTCGATGAAGAATTTAATCATTC 	AGATTATTTGCCAAAGGCTGTTTTTTCAGAGT 	IGAACCACCTGGTAAAGAAATGAAACAGAACGC 	TAAAATTGTGAAAGAAAAGGTACCTTACATCTATK 	RATTCATAGAATACCTTTAGTTTCTATTAT. 	ICAAAGATGTGTAGATAGTGCTCTTAATCAA 	ITAACGATGGTTCAACAGATAATACCTTAGAAGTC 	AGGGTACGCATCATGTCTAAACCAAATGG
GTTCTTGCTCCATTGCCAGATCATC	AGCTTAGGTATAAAGCCTGTAAATAAG 	AATCGTAGCCGTATTTTAGATATAACGTT	CCATTIGAAGTCGTIGTTGCAGAT	AAATACGAACAAAACTT	TGTGCAGTCAGAAACTTAGGTTTACC	TGCGATATGGCACCACAACAATTATG 	AATGATATTGTTTAATTC 	CAATTCCTTAACGATCCATAT	1 CCTTCGATTACATCAAAAGGAAATATATGTTT 	ACCGATAATCTACGTCTATGTGATTC	1 TTTCTAAAGAATGGCTAAATAAAGTAGGTTG 	1 GGCGAAGATGTAGAATTTGGTTACAGATT 	GACGGCGGAATGGCCATCCATCAAGAACCACTGG	1 GCTGGTAAAGTATTACGCT 	1 CTTTTACCAATAGAAGATTCACATATTC 	1 GCTTATAACTGTGCAAATTATATTTCAAAGAT(GTCGATCTCGAGGTTTGTATTTG 	1 AATAAGCTTTATGGTAATAATCC
421	481	541	601	661	721	781	841	901	961	1021	1081	1141	120]	126.	132	138.	144	0
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1560 1620 1620	1680	1740	1800	1860	1920	1980 1980	2040	2100	2160	2220	2280 2280	2340 2340	2400	2460	2520	2580	2640
	21 TC 21 TC 21 TC	1681 AAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTCAATCCGGATGGTAGCTTAATC 	1741 GCTAATGGTTACAATTGGCCAGAATTTTCACGAGAAAAACTCACAACGGCTATGATTGCT 	01 CACCATTTA 01 CACCATTTA	861 861	1921 CATCTTAATAAAATCTGCTATAACGGGGTATTACATGGTGATAACACATCCATTAAGAAA 	1981 CTCGGCATTCAAAAGAAAAACCATTTTGTTGTAGTCAATCAGTCATTAAATAGACAAGGC	2041 ATCAATTATTATAATTATGACAAATTTGATGATTATAGATGAAAGTAGAAAGTATATCTTC 2041 ATCAATTATTATAATTATGACAAATTTGATGATTTAGATGAAAGTAGAAAGTATATTTG	2101 AATAAAACCGCTGAATATCAAGAAAATGGATATĞTTAAAAGATCTTAAACTCATTCAA 1111111111111111111111	2161 AATAAAGATGCCAAAATCGCAGTCAGTATTTTCTATCCCAATACATTAAACGGCTTAGTG 2161 AATAAAGATGCCAAAATCGCAGTCAGTATTTTCTATCCCAATACATTAAACGCTTAGTG	2221 AAAAAACTAAACAATATTATTGAATATAAAAATATATATTGGTTATTGTTGT	2281 GATAAGAATCATCTTACACCAGACATCAAAAAAGAAATATTGGCTTTCTATCATAAGCAC 	2341 CAAGTGAATATTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTAATAAAA 	401 ACTGAGGCACATTTA 	2461 ATCATTTTTGATAATCATGACAGCCTATTCGTTAAAAATGACAGCTATGCTTATATGAAA 	2521 AAATATGATGTCGCCATGAATTTCTCAĞCATTAACACATGATTGGATCGAGAAAATCAAT 	2581 GCGCATCCACCATTAAAAAGCTGATTAAAACCTATTTAATGACAATGACTTAAGAAGT
Db Db	Qy Dp	Qy	Qy	δy	QY Dp	Qy Db	Qy Db	Qy Up	oy Dp	Qy	Qy	Qy Db	δλ	QY	Qy Db	Qy	Qy

us-09-842-484a-1.rni

AAAGATTTTCCTAAAGATCTTGTTCTTGCTCCATTGCCAGATCATGTTAATGATTTTACA	580 GTCAATCAGAAACAACTACCCATTTGAAGTCGTTGTTGCAATGATGGTAGTAAGGAA 639	700 AAAGATTATGGATATCAATTGTGTGCAGTCAGAAACTTAGGTTTACGTACAGCAAAGTAT 759	CTTACAGAACTATTAGAAGAATGATATTGTTTTAATTGGACCTAGAAATATGTGGAT	841 ACACAACATATTGACCCCAAAGACTTCTTAAATAACGCGGGTTTGCTTGAATCATTACCA 900 940 GAAACCGCTACAAATAACAATCCTTCGATTACATCAAAAGGAAATATATCGTTGGATTGG 999 11		1060 TTTGTTGGGGGTAATGTTGCATTTTCTAAAGAATGGCTAAATAAA	GAAGAATTTAATCATTGGGGGGGGGGGAAGATGTAGAATTTGGTTACAGATTATTGCCAAA 	1180 GGCTGTTTTTTCAGAGTAATTGACGGCGGAATGGCCATCCAT	1240 GAAAATGAAACAGAACGCGAAGCTGGTAAAAGTATTACGCTTAAAATTGTGAAAGAAA	1300 GTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCACATATTCATAGAATACCT 1359 	1360 TTAGTTTCATTTATATCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGTAGAT 1419 	1420 AGTGCTCTTAATCAAACTGTTGTGCGATCTCCAGGTTTGTAATTGTAACGATGGTTCAACA 1479
\(\delta \) \(\de	& a & a	9 O O	& & &	ος Α	Qy Db	ov Ov		QQ Op	Qy	QY	Qy	QY
GCGCATCCACCATTAAAAAGCTGATTAAAACCTATTTAATGACAATGACTTAAGAAGT 2640	AACACTGAGGATATTTGGTTCCAATTTGCACTTTTAATCTTAGAAAGAA		SULY 2 1-09-437-277-2 1-09-437-277-2 1-09-437-277-2 1-09-437-277-2 1-09-437-277-2 1-09-437-277-2 1-09-437-277-2 1-09-437-277-2 1-09-437-277-2 1-09-437-277-2 1-09-437-277-2 1-09-437-277-2 1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1	; FILE KREKENEN: 3820.351 CURRENT APPLICATION NUMBER: US/09/437,277 CURRENT FILING DATE: 1999-11-10 NUMBER OF SEQ ID NOS: 6 SOFTWARE: WordPerfect 8.0 (saved in ASCII format)	SEQ ID NO 2 LENGTH: 2112 TYPE: DNA ORGANISM: Pasteurella multocida -09-437-277-2	Similarity 82.5%; Score 1503.2; DB 4; Length 2112; Similarity 82.5%; Pred. No. 0; 3; Conservative 0; Mismatches 348; Indels 21; Gaps 1;	CAATAAAAGCATATAACAGCAATGACTATGAATTAGCACTC 120	AAATTATTTGAGAAGTCTGCTGAAACCTACGGGGGAAAATGGTTGAATTCCAAATTATC 180 	TAAGT	TACTT	AATGG	

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1660 TTAAAAGAATTTTTAAAAGATAAAACGCTAGCTTGTGTTTTATACCACTAATAGAAACGTC 1719
                                                                                                                                                                             1840 ACGGATGGATTTAACGAAAATATTGAAAACGCCGTGGATTATGACATGTTCCTTAAACTC 1899
                                                                                                                                                                                                                                                                                                                                                           1900 AGTGAAGTTGGAAAATTTAAACATCTTAATAAAATCTGCTATAACCGGGTATTACATGGT 1959
                                                                                                                                                                                                                                                                                                                                                                                                                    2020 CAGTCATTAAATAGACAAGGCATCAATTATTATAATTATGACAAATTTGATGATTTAGAT 2079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2080 GAAAGTAGAAAGTATATCTTCAATAAAACCGCTGAATATCAAGAAGAAATGGATATGTTA 2139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1441 GATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGCATCATG 1500
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                                          Sequence 1, Application US/08597236
Fatent No. 5733765
GENERAL INFORMATION:
APPLICANT: WOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION:
CORRESPONDENCES: 19
CORRESPONDENCES: 19
CONDERSPONDENCES: 19
COUNTRY: US.A.
ZIPT: New YORK
COUNTRY: US.A.
ZIPT: 10036
COMPUTER: Floppy disk
COMPUTER: PIP PROCOMPATIBLE
COMPUTER: PATENTINE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION NATA:: US/08/597,236
FILING DATE:
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2101 AAAGATATTTAA 2112
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NAME/KEY: misc_feature
LOCATION 11302..1222
OTHER INFORMATION: (PS k) on nucleotides 10392-11339"
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LOCATION: 13732.14305
OTHER INFORMATION: /function= "CDS on the
OTHER INFORMATION: complementary strand"
OTHER INFORMATION: /product= "orfz"
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci A., Allan
REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14602 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
TOPOLOGY: Linear
TOPOLOGY: Linear
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LOCATION: 6425..7540
OTHER INFORMATION: /product= "epsG"
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NAME/KEY: CDS
LOCATION: 7736.8212
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LOCATION: 8221..9192
OTHER INFORMATION: /product= "epsl"
FEATURE:
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LOCATION: 9285..10364
OTHER INFORMATION: /product= "epsJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: CDS
LOCATION: 10392..11339
OTHER INFORMATION: /product= "epsk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 12233..13651
OTHER INFORMATION: /product= "epsm"
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LOCATION: 3249..3995
OTHER INFORMATION: /product= "epsD"
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LOCATION: 352..1803
OTHER INFORMATION: /product= "epsa"
FEATURE:
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LOCATION: 4898..5854.
OTHER INFORMATION: /product=
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LOCATION: 2547..3239
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                   1403 TTCAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTT 1462
                                                                                                                                                                                                                                                                                                                                                                     1583 TTTCTTTTGCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTG 1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8459 TTAAAAAGGCTAAAGGATCGTTTATCACATTTGTAGATAGTGATGACTACATAGTAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1643 ATGCAGTIGAACTGTGTTTAAAAGAATTTTTAAAAGATAAAACGCTAGCTTGT 1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8519 ATTATCTTTCTCATTTGGTAGCTGGGATAAAAGTGAGACCTCTATAGTTTGT 8571
                                                                                                                                                                                               Query Match 2.5%; Score 74.6; DB 1; Length 14602; Best Local Similarity 50.7%; Pred. No. 1e-07; Matches 179; Conservative 0; Mismatches 174; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,682A
FILING DATE: 14-NOV-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/597,236
FILING DATE: 20-JUN 1995
APPLICATION NUMBER: BP 95201669.9
FILING DATE: 20-JUN 1995
APPLICATION NUMBER: BP 95201669.9
FILING DATE: 20-JUN 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: STINGELE, Franscesca
APPLICANT: STINGELE, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXOPOLYSACCHARIDES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-746-682A-1
: Sequence 1, Application US/08746682A
; Patent No. 5786184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fanucci A., Allan
                  terminator
                                                                       promoter
274..302
                                                                                                                                        340..345
                                   230..252
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                 NAME/KEY:
LOCATION:
FEATURE:
                                                                      NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                         ; NAME/KEY;
; LOCATION:
US-08-597-236-1
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LOCATION: 11302..1223
OTHER INFORMATION: /product- "CDS (eps L) covering CDS
OTHER INFORMATION: (eps k) on nucleotides 10392-11339"
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LOCATION: 13732..14305
OTHER INFORMATION: /function= "CDS on the
OTHER INFORMATION: complementary strand"
OTHER INFORMATION: /product="orfz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 10392..11339
OTHER INFORMATION: /product- "epsk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 12233..13651
OTHER INFORMATION: /product- "epsm"
FEATURE:
                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 1807..2535
OTHER INFORMATION: /product= "epsB"
                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 2547..3239
OTHER INFORMATION: /product= "epsC"
                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 3249..3995
OTHER INFORMATION: /product= "epsD"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 4051..4731
OTHER INFORMATION: /product- "epsE'
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 4898..5854
OTHER INFORMATION: /product= "epsF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 6425.7540
OTHER INFORMATION: /product= "epsG"
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LOCATION: 7736..8212
OTHER INFORMATION: /product- "epsH"
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LOCATION: 8221..9192
OTHER INFORMATION: /product- "eps!"
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NAME/KEY: CDS
LOCATION: 9285..10364
OTHER INFORMATION: /product= "epsJ"
FEATURE:
                                                                                                                                                                                                                         /product- "epsA"
REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14602 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 3249..3995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 4898..5854
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230..252
                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 352..1803
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FEATURE:
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NAME/KEY:
LOCATION:
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LOCATION:
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Mon Jan 6 18:39:49 2003
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                                                                                                                                                             8219 AAATGTATCT¶AAAAGTCTAATCTCTATTGTTATTCCAGTATATAATGTAGAGAAATAT 8278
                                                                                                                                                                                                 1403 TICAAAGAIGIGTAGAIAGIGCICITAAICAAACIGIIGICGAICICGAGGITIGIAIII 1462
                                                                                                                              1343 ATATICATAGAATACCITTAGITICIATITATATCCCCGCITATAACIGIGCAAAITAIA 1402
                                                                                              Gaps
                                                                                                                                                                                                                                                                   1463 GTAACGATGGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATC
                                                                                                                                                                                                                                                                                                                                                            TTTCTTTTGCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                            1643 ATGCAGTTGAACTGTGTTTAAAAGAATTTTTAAAAGATAAAACGCTAGCTTGT 1695
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                                                            Length 14602;
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF/5-30306/A/CGC1976
                                                            Score 74.6; DB 1;
Pred. No. 1e-07;
0; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: NO. 6239264artis Corporation
1: 3054 Cornwallis Road
Research Triangle Park
1: No. 6239264th Carolina
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUI
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 186, Application US/08998416 Patent No. 6239264
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
                                                                2.5%;
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 RBS 340..345
                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-998-416-186/c
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STREET: 305
CITY: Resea
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
; NAME/KEY:
; LOCATION:
US-08-746-682A-1
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                                                                                                    Matches 179;
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                                                                   Query Match
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                                                                                                                                                                                                                                                                                           2019 ICAGTCATTAAATAGACAAGGCATCAATTATATAATTATGACAAATTTGATGATTTAGA 2078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2199 CAATACATTAAACGGCTTAGTGAAAAAACTAAACAATATTATTGAATATAAAAAATAT 2258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2079 TGAAAGTAGAAATATATTTCAATAAAACCGCTGAATATCAAGAAGAAATGGATATGTT 2138
                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 TATATTAATTATTGATAATCTATTTAATAATTTAAAGAAAATAATAATAATAA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 TATTITAATAACTAATTTAAAATTTGAACATAGACTAAATAGTATTCATATTAAATATA 192
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                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Philippsen, Peter
APPLICANT: Philippsen, Rainer
APPLICANT: Pollmann, Rainer
APPLICANT: Pollmann, Rainer
APPLICANT: Mohr, Christine
APPLICANT: Wenchland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 6722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3319 ATTGGCTTTCTATCATAAGCACCAAGTGAATATTTTACTAAATAATGACATCTCATATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                  491 ATAAGAAATTAAAGTTAAAATTAATTTTAATAATAATTCTTATAAAAAGTTAAATAATAT
                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                       Length 615;
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                       Score 74.2; DB 4;
Pred. No. 4.8e-08;
0; Mismatches 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2499 TGACAGCTATGCTTATATGAAAAAATATGAT 2529
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                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                           Query Match 2.5%;
Best Local Similarity 46.6%;
Matches 238; Conservative
                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomi
: 919-541-8587
919-541-8689
                    TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                         ORGANISM: PAG1074RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-998-416-288/c
                                                                                                                                                                                             US-08-998-416-186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 TTATTAAATAATAAAAATTAATAATAAGAAATT--AAAGTTAAAAATTAATAA 460
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Pred. No. 3.4e-07;
0; Mismatches 284; Indels
                                                                                                                              SOFTWARE: PATENTIA PLOYMENT #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 288: SEQUENCE CHARACTERISTICS: LENGTH: 877 base pairs TYPE: nucleic acid STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
2.4%;
Best Local Similarity 46.9%;
Matches 253; Conservative (
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAG1241RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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US-08-998-416-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                      COUNTRY:
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1999 AACCATTTTGTTGTTGTAGTCAATCAGTCATTAAATAGACAAGGCATCAATTATTATAATTAT 2058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2179 GCAGTCAGTATTTCTATCCCAATACATTAAACGGCTTAGTGAAAAAAACTAAACAATATT 2238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         564 AAATAATTAATTAAATAAATAAATAAATAAATAAAATGAATATAATTAATTAAATA 505
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APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Rebischung, Corinne
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: 1152
CORRESPONDENCE: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 273; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 70.2; DB 4;
Pred. No. 3.9e-07;
                                                                                                                                                                                                                                                                                                                                          SEE: No. 6239264artis Corporation

1: 3054 Cornwallis Road

Research Triangle Park

No. 6239264th Carolina
Patent No. 6239264
GRWDAY ---- 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timchy
REGISTRATION NUMBER: 38, 241-30
REFERENCE/DOCKET NUMBER: PF/5-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1137:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 919-541-8587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.4%;
Best Local Similarity 47.3%;
Matches 251; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: PAG1692RP
US-08-998-416-1137
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ORIGINAL SOURCE:
US-08-998-416-1137/C
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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COUNTRY:
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1854 CGAAAATTTGAAAACGCCGTGGATTATGACATGTTCCTTAAACTCAGTGAAGTTGGAAA 1913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6261 AACATATAAAAATATTGAGATTGTTGTCGTTAATGATGGTTCTACGGATGCTTCAGGTGA 6320
                                                                                                                                                                                                                                                                                                                            1674 AAAAGATAAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTCAATCCGGATGGTAG 1733
                                                                                                                                                                                                                                                                                                                                                                      AGAGTATCAGGCTGATATTGCAGTTGGTAATTATTATTCTTTCAACGAAAGTGAAGGAAT 6560
                                              1494 AGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGCATCATGTCTAAACCAAATGG
                                                                                       6321 AATTTGTAAAGAATTTTCAGAAATGGATCACCGAATTCTCTATATAGAACAAGAAAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                       1734 CITAATCGCTAATGGTTACAATTGGCCAGAATTTTCACGAGAAAAACTCACAACGGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6621 CTTTGAGAACTTGTATGAAACTCAAGAAATGAAGAGTTTTGCTTTGATATCTGCTTGGGG
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                                                                                                                                                                                                                                     1614 GITAGATICAGATGATTATCITGAGCCTGATGCAGTTGAACTGTGTTAAAAGAATTTTT
                                                                                                                                                                                                                                                             6561 GTTCTACTTTCATATTGGGAGACTCCTATTATGAGAAAGTATATGATAATGTTTCTAT
                                                                                                                                                                                    6381 TGGTCTTTCTGCCGCACGAAACACCGGTCTGAATAATATGTCCGGAAATTATGTGACCTT
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APPLICANT: Patrick E. Duffy
APPLICANT: Christian F. Ockenhouse
TITLE OF INVENTION: SEQUESTRIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: Macintosh 7.5 SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,89
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STREET: USA MRMC -JA
CITY: FORT DETRICK, FREDERICK
STATE: MARYLAND
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REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintos
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-08-559-896B-1
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Sequence 71. Application US/08961527

Patent No. 6420135

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
ATITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
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                                                                                                                                                                                                                                                                                          AATATTAATAAATTAAGTCAGTTAAATCTAAATTGTGAATACATCATTTTTGATAATCAT 2478
                                                                                                                                                                                                   2418
         2239 ATTGAATATAATAAAAATATATTCGTTATTATTCTACATGTTGATAAGAATCATCTTACA 2298
                                                     331 AATAAACAATTAATAAATATATTAATTATTGATAATCTATTTAATAATTTAAAG 272
                                                                                                                                                    271 AAAATAATAATATATATAATAATATTTAATAACTAATTTAAAAATTGAACATAGACTAAAT 212
                                                                                                                                                                                                                                            2299 CCAGACATCAAAAAAGAAATATTGGCTTTCTATCATAAGCACCAAGTGAATATTTTACTA
                                                                                                                                                                                                   AATAATGACATCTCATATTACACGAGTAATAGACTAATAAAAACTGAGGCACATTTAAGT
                                                                                                                                                                                                                                                                                                                                         2.3%; Score 67.2; DB 4; Length 32768; ilarity 44.9%; Pred. No. 6e-06; Conservative 0; Mismatches 313; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                       2479 GACAGCCTATTCGTTAAAATGACAGCTATGCTTATATGAAAAAATATGAT 2529
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
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REGISTATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB341
TELECOMMUNICATION INFORMATION:
TELEPAN: (301) 309-8504
TELEPAN: (301) 309-8512
INFORMATION FOR SEO ID NO: 71:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 32768 base pairs
nucleic acid
EDNESS: double
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity
255; Conserva
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US-08-961-527-71
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Matches 25
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single
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US-08-961-527-86/c
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APPLICANT: Sim, Kim L.
APPLICANT: Chituis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
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                                                                                                                                                                          1987 ATTCAAAAGAAAACCATTTTGTTGTAGTCAATCAGTCATTAAATAGACAAGGCATCAAT 2046
                                                                                                                                                                                                                                                                                                                                                     1348 CGAAATTTAGACAAGGATAAAGGAGCCAAGATAGAAGATATTATAGACTATTTTAACAAA 1407
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                                                                                                                                                                                                                                                  2047 TATTATAATTATGACAAATTTGATGATTTAGATGAAAGTAGAAAGTATATCTTCAATAAA 2106
                                                                                                                                                                                                                                                                                       1288 TTAAATAATAAGCACACAAATAATAATTATAAAGAAATGTAGAAGTTGAATTAGTTGTA 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAATTAAAAAAGACAAAAATGTTAATGTTTCCAATATAGTGAATTTTTTAAATTCAAAA 1467
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                                                                                                                                                                                                              AAAAATATTCAGATTATTCAAGAGGATAATATAAAAATAAAGGCCAAAAGGATAACACT 1587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2227 CTAAACAATATTATTGAATATAAAAAATATATTCGTTATTATTCTACATGTTGATAAG
                                                                                                                                                                                                                                                                                                                               ACCGCTGAATATCAAGAAGAAATGGATATGTTAAAAGATCTTAAACTCATTCAAAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                         GATGCCAAAATCGCAGTCAGTATTTTCTATCCCAATACATTAAACGGCTTAGTGAAAAA
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                                                                                              Score 66.8; DB 4; Length 1956;
Pred. No. 3.2e-06;
0; Mismatches 317; Indels 6
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STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
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                                                                                              Query Match 2.2%;
Best Local Similarity 45.8%;
Matches 273; Conservative (
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MEDIUM TYPE: Floppy disk
TYPE: Nucleic acid
STRANDEDNESS: Double
                STRANDEDNESS:
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US-08-559-8968-1
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Streptococcus pneumoniae Polynucleotides and Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1972 ATTAAGAAACTCGGCATTCAAAAGAAAAACCATTTTGTTGTTGTAGTCAATCAGTCATTAAAT 2031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2032 AGACAAGGCATCAATTATATAATTATGACAAATTTGATGAT-TTAGATGAAAGTAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2151 ACTCATTCAAAATAAAGATGCCAAAATCGCAGTCAGTATTTTCTATCCCAATACATTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGCTTAGTGAAAAAACTAAACAATATTATTGAATATAAAAAATATATTCGTTATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 63.2; DB 2; Length 1 Pred. No. 4.1e-05; 0; Mismatches 273; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/487,826B FILING DATE: 10-SEP-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 86, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptcoccus
                                                                                        FILING DATE: LV CL.
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIHIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.1%;
Best Local Similarity 47.5%;
Matches 250; Conservative
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422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1473 TTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACG 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4465 TGCAACAGATGAAAGTGGTCGCTTGTGTGATTCAATCGCTGAACAAGATGACAGGGTGTC 4406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1593 TAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGA 1652
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APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 19390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.00013;
0; Mismatches 175; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4285 GAGCITATATGAGCAATTAGTICAAGAAGATGCGGATGTTT 4245
                                                                                                                  ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                               ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 61;
Pred. No. 0
                                                                                                                                                                                      OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII TEAX
CURRENY APPLICATION DATA: APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                   NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-961-083-199
; Sequence 199, Application US/08961083
; Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.0%;
Best Local Similarity 48.7%;
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 19390 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NUMBER OF SEQUENCES: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                double
                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                    Maryland
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                                                                                                                                                                                                                                                               FILING DATE:
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US-08-961-527-8
                                                                                                     COUNTRY:
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.651 GAACIGIGITITAAAAGAATITITAAAAGATAAAACGCTAGCTIGIGITITATACCACTAAI 1710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1831 TGGCATTTAACGGATGGATTTAACGAAAATATTGAAAACGCCGTGGATTATGACATGTC 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTT 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1411 IGTGTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGAT 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1471 GGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTA 1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 TCTTTCAACGAAAGTGAATGTTCTACTTTCATATATGGGAGACTCCTATTATGGG 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1591 GCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 GAAACTCTATATAAAAAATAGTAGGATATCAGGCTGATATTGCAGTTGGTAATTATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 CICTATATAGAACAAGAAAATGCIGGICITTCIGCCGCACGAAACACCGGICIGAATAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITAAACTCAGTGAAGTTGGAAAATTTAAACATCTTAATAAAATCTGCTAT 1941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2023;
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WEDTUTR READABLE FORM:
MEDIOM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 60.6; DB 3;
Pred. No. 8.1e-05;
0; Mismatches 294;
Sciences, Inc.
                                                                                                                                                                                           SUFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNOW AND ATTORNOW AND ATTORNOW AND ATTORNOW A
                                                                                                                                                                                                                                                                                                                                                                                                       FILLING DAALE:
ATTORNEY/GENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36.33
REFERENCE/DOCKET NUMBER: PB340P2
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 2023 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.0%;
44.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.0 Best Local Similarity 44.6 Matches 237; Conservative
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STRANDEDNESS: double
  E: Human
9410 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                    Maryland: USA
                        STREET: 9410 Key CITY: Rockville
  ADDRESSEE:
                                                                    STATE: Ma
COUNTRY:
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2341 CAAGTGAATATTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTAATAAAA 2400
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COMPUTER READABLE FORM:
COMPUTER: ISH PC compatible
COMPUTER: ISH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.9%; Score 57.8; DB 2; 45.0%; Pred. No. 0.00048;
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NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 6243 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 300; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: W
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2221 AAAAAACTAAACAATATTATTGAATATAAAAAATATATTGGTTATTATTCTACATGTT 2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2281 GATAAGAATCATCTTACACCAGACATCAAAAAAGAAATATTGGCTTTCTATCATAAGCAC 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2101 AATAAAACCGCTGAATATCAAGAAGAAATGGATATGTTAAAAGATCTTAAACTCATTCAA 2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        547 AATAAAATAGAAATAGAAATAGCATATATTATTATGTTCACAAAATACAATCTATATAATG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.0%; Score 58.8; DB 4; I
Best Local Similarity 48.0%; Pred. No. 0.00015;
Matches 168; Conservative 0; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
CATTE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US./08/998,416
FILING DATE: 24-DEC-1997
CLASSIPICATION ATA:
APPLICATION NATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATOONEY/AGENT INFORMATION:
NAME: Meligs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306,
TELEPHONE: 919-541-8587
                                    US-08-998-416-595/c
: Sequence 555, Application US/08998416
: Patent No. 6239264
: GENERAL INFORMATION:
: APPLICANT: Philippsen, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                      Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 595:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 658 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAG1408RP
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US-08-998-416-595
                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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1852 AACGAAAATATTGAAAACGCCGTGGATTATGACATGTTCCTTAAACTCAGTGAAGTTGGA 1911
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NAME/KEY: misc_feature
LOCATION: 3770..4013
OTHER INFORMATION: /note= "RP4 origin of DNA transfer (oriT) from
OTHER INFORMATION: plasmid RP4"
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                                                       2401 ACTGAGGCACATTTAAGTAATATTAATAAATTAAGTCAGTTAAATCTAAA 2450
                                                                                    Sequence 1, 4/2
Sequence 1, 4/2
Patent No. 595386
GENERAL INFORMATION:
APPLICANT: Johnson, Eric A.
APPLICANT: Broad, Julian:
TITLE OF INVENTION: Expression System for Clostridium:
TITLE OF INVENTION: Species
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 362; Indels
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                         2152 CTCATTCAAAATAAAGATGCCAAAATCGCAGTCAGTATTTTCTATCCCAATACATTAAAC 2211
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                                                                                                                                                                                                                                                                       2332 CATAAGCACCAAGTGAATATTTACTAAATAATGACATCTCATATTACACGAGTAATAGA 2391
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2032 AGACAAGGCATCAATTATTATAATTATGACAAATTTGATGATTTAGATGAAAGTAGAAAG 2091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 197, Application US/08961083
Sequence 197, Application US/08961083
Patent No. 6159469
GENERAL INPORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2452 TGTGAATACATCATTTTTGATAATCATGACAGCCTATTCGTTAAAAATGACAGCTATGCT
                                                                                                                                                                                                                                                  2212 GGCTTAGTGAAAAAACTAAAACTAATATTTGAATATAATAAAAAATATTTGTTATT
                                                                                  2092 TATATCTTCAATAAAACCGCTGAATATCAAGAAGAAATGGATATGTTAAAAGATCTTAAA
                                                                                                                                                                                                                                                                                                                                                                           2982 TAAAAACTAAAATTAGTAAATCATCTAAATATTACAAATGAAGAAATATTATTTGTAAAT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MSDOS version 6.2
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brookes, A. Anders
REGLETRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 197:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                          1531 CGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTT 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                       1591 GCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTT 1650
                                                                                                                                                                                                                                                                                                        62 GGCTCTCCAGATCATCATCCAAAATATGTGAAGAATTTGTAGAGAAGATCTCGTTTC 121
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                                                                                                                                                             ;
0
                                                                                                                  Length 811;
                                                                                                                                                             Indels
                                                                                                                  Score 57.6; DB 3;
Pred. No. 0.00029;
0; Mismatches 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 GACCGATTATATGGTGCTTTGAAAAAGGAAAA 273
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ne : 314 secs
                                                                                                                          1.9%;
; LENGTH: 811 base pairs
; TYPE: nucleic acid
; STRANBEDNESS: double
; TOPOLOGY: linear
US-08-961-083-197
                                                                                                                          Query Match
Best Local Similarity 50.7%
Matches 138; Conservative
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January 3, 2003, 23:56:15 ; Search time 168 Seconds (without alignments) 7669.230 Million cell updates/sec
                                                                                                                                                                                   US-09-842-484A-1
2979
1 ttataaaactgattaaagaag.....acatttgcattttattaaaa 2979
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                    381593 seqs, 216252194 residues
                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                               IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                   Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                            Run on:
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763186

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Databa

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

	Published_Applications_NA:* 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:* 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:* 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:* 4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:* 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:* 6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:* 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:* 8: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:* 9: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:* 10: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:* 11: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:* 11: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:* 12: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:* 13: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:* 13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description			90				
1 2283.4 76.6 2937 9 0S-09-879-959-9 8 8 8 2.9 5550 10 US-09-070-927A-137 8 9 0.6 2.7 1685 10 US-09-070-927A-137 8 9 0.6 2.7 1685 10 US-09-070-927A-137 8 74.2 2.5 17276 9 US-09-870-759-83 6 73.2 2.5 17276 9 US-09-870-759-83 6 8 4 2.3 891 10 US-09-767-041-9 6 6 8 2.2 1956 10 US-09-767-041-9 6 6 8 2.2 1956 10 US-09-816-028A-28 11 66.6 2.2 1956 10 US-09-816-028A-28 12 6 10 US-09-816-028A-28 13 6 0.6 2.0 2023 10 US-09-765-277-199 14 58.6 2.0 431 10 US-09-960-352-5558 15 57.6 1.9 40881 10 US-09-765-272-197 18 55 1.8 3876 12 US-10-051-952-3400	Result No.	Score	Query Match	Length	DB	ID	Description
2 86 2.9 5550 10 US-09-070-927A-137 4 79.2 2.7 11474 10 US-09-00038A-3 5 74.2 2.5 17276 9 US-09-8016-028A-1 6 73.2 2.5 6992 10 US-09-767-041-29 8 68.4 2.3 6992 10 US-09-767-041-29 9 67.2 2.3 991 10 US-09-767-041-29 10 66.8 2.2 1956 10 US-09-767-041-29 11 66.6 2.2 1956 10 US-09-16-028A-28 12 61.8 2.1 2406 10 US-09-016-028A-26 13 60.6 2.0 2023 10 US-09-765-277-199 14 58.6 2.0 431 10 US-09-765-272-199 15 57.6 1.9 640681 10 US-09-765-272-197 18 55 1.8 876 12 US-09-765-272-197 19 55 1.9 640681 10 US-09-988-1 19 55 1.8 3876 12 US-10-051-952-4	-	2283.4	76.6	2937	6	US-09-879-959-9	Sequence 9, Appli
3 80.6 2.7 6865 10 US-09-000-038A-3 5 74.2 2.5 11274 10 US-09-08.028A-1 6 73.2 2.5 17276 9 US-09-870-759-83 7 73.2 2.5 6992 10 US-09-767-041-9 8 67.2 2.3 912 10 US-09-767-041-29 9 67.2 2.3 912 10 US-09-16-028A-30 10 66.8 2.2 1956 10 US-09-816-028A-26 11 66.6 2.2 996 10 US-09-816-028A-26 12 61.8 2.1 2406 10 US-09-151-794A-1 14 58.8 2.0 2023 10 US-09-35-785 15 51.9 40081 10 US-09-765-272-199 16 57.6 1.9 411 10 US-09-765-272-197 17 56 1.9 64081 10 US-09-765-272-197 18 55 1.8 3876 12 US-10-051-952-4	7	86	2.9	5550	10	US-09-070-927A-137	Sequence 137, App
4 79.2 2.7 11474 10 US-09-016-028A-1 5 74.2 2.5 6992 10 US-09-870-759-83 7 73.2 2.5 6992 10 US-09-767-041-29 8 68.4 2.3 891 10 US-09-767-041-29 9 67.2 2.3 912 10 US-09-16-028A-28 10 66.8 2.2 1956 10 US-09-16-028A-26 11 66.6 2.2 906 10 US-09-351-794A-1 13 60.6 2.0 2023 10 US-09-351-794A-1 14 58.8 2.0 2023 10 US-09-352-785 15 57.6 1.9 64081 10 US-09-765-272-199 16 57.6 1.9 64081 10 US-09-765-272-197 19 55 1.9 64081 10 US-09-765-272-197 19 876 12 US-10-9732-3400 19 876 12 US-10-952-3400	e	90.6	2.7	6865	10	US-09-900-038A-3	Sequence 3, Appli
17276 9 US-09-870-759-83 Si 6992 10 US-09-767-041-9 6992 10 US-09-767-041-9 891 10 US-09-816-028A-30 912 10 US-09-816-028A-28 1956 10 US-09-816-028A-26 2406 10 US-09-816-028A-26 2406 10 US-09-765-272-199 516 10 US-09-765-272-199 516 10 US-09-765-272-197 841 10 US-09-765-272-197 640681 10 US-09-766-35-8 811 10 US-09-766-35-8 814 10 US-09-760-352-3400 3876 12 US-10-051-952-3	O 4	79.2	2.7	11474	10	US-09-816-028A-1	Sequence 1, Appli
6992 10 US-09-767-041-9 6992 10 US-09-767-041-9 891 10 US-09-767-041-29 891 10 US-09-816-028A-28 1956 10 US-09-816-028A-28 2406 10 US-09-816-028A-26 2406 10 US-09-765-272-199 516 10 US-09-765-272-199 516 10 US-09-765-272-197 8481 10 US-09-765-272-197 8446 10 US-09-766-355-8 811 10 US-09-766-352-3400 3876 12 US-10-051-952-3400	S	74.2	2.5	17276	6	US-09-870-759-83	Sequence 83, Appl
6992 10 US-09-767-041-29 891 10 US-09-816-028A-28 1956 10 US-09-816-028A-28 906 10 US-09-816-028A-26 2023 10 US-09-816-028A-26 2023 10 US-09-076-927A-308 516 10 US-09-765-272-199 516 10 US-09-960-352-5785 811 10 US-09-960-352-5785 811 10 US-09-960-352-3400 3476 12 US-10-051-952-4	9	73.2	2.5	6992	10	US-09-767-041-9	-
891 10 US-09-816-028A-30 912 10 US-09-816-028A-28 1956 10 US-09-816-028A-28 2406 10 US-09-816-028A-26 2023 10 US-09-765-272-199 516 10 US-09-765-272-199 431 10 US-09-960-352-558 811 10 US-09-765-272-197 640681 10 US-09-760-388-1 446 10 US-09-960-352-3400 3876 12 US-10-051-952-3	7	73.2	2.5	6992	10	US-09-767-041-29	Sequence 29, Appl
912 10 US-09-816-028A-28 1956 10 US-09-351-794A-1 906 10 US-09-351-794A-1 2406 10 US-09-070-927A-308 2023 10 US-09-765-272-199 516 10 US-09-960-352-5785 431 10 US-09-960-352-558 811 10 US-09-765-272-197 640681 10 US-09-760-352-3400 3876 12 US-10-051-952-3400	80	68.4	2.3	891	10	US-09-816-028A-30	Sequence 30, Appl
1956 10 US-09-351-794A-1 906 10 US-09-816-028A-26 2406 10 US-09-070-927A-308 2023 10 US-09-765-272-199 516 10 US-09-960-352-5785 431 10 US-09-960-352-558 811 10 US-09-765-272-197 640681 10 US-09-766-352-3400 3476 12 US-10-051-952-34	σ	67.2	2.3	912	10	US-09-816-028A-28	Sequence 28, Appl
906 10 US-09-816-028A-26 2406 10 US-09-070-927A-308 2023 10 US-09-076-272-199 516 10 US-09-960-352-5785 431 10 US-09-960-352-558 811 10 US-09-765-272-197 640681 10 US-09-760-388-1 446 10 US-09-960-352-3400 3876 12 US-10-051-952-4	10	8.99	2.2	1956	10	US-09-351-794A-1	1, A
2406 10 US-09-070-927A-308 2023 10 US-09-765-272-199 516 10 US-09-960-352-5785 431 10 US-09-960-352-558 811 10 US-09-765-272-197 640681 10 US-09-765-272-197 446 10 US-09-760-352-3400 3876 12 US-10-051-952-4	11	9.99	2.5	906	10	US-09-816-028A-26	26,
2023 10 US-09-765-272-199 516 10 US-09-960-352-5785 431 10 US-09-960-352-558 811 10 US-09-765-272-197 640681 10 US-09-790-988-1 446 10 US-09-960-352-3400 3876 12 US-10-051-952-4	c 12	61.8	2.1	2406	10	US-09-070-927A-308	Sequence 308, App
516 10 US-09-960-352-5785 431 10 US-09-960-352-5558 811 10 US-09-765-272-197 640681 10 US-09-790-988-1 446 10 US-09-960-352-3400 3876 12 US-10-051-952-4	13	9.09	2.0	2023	10	US-09-765-272-199	Sequence 199, App
431 10 US-09-960-352-5558 811 10 US-09-765-272-197 640681 10 US-09-790-988-1 446 10 US-09-960-352-3400 3876 12 US-10-051-952-4	c 14	58.8	2.0	516	10	US-09-960-352-5785	٠,
1 10 US-09-765-272-197 10 US-09-790-988-1 10 US-09-960-352-3400 12 US-10-051-952-4	c 15	58.6	2.0	431	10	US-09-960-352-5558	Sequence 5558, Ap
1 10 US-09-790-988-1 5 10 US-09-960-352-3400 5 12 US-10-051-952-4	16	57.6	1.9	811	10	US-09-765-272-197	Sequence 197, App
10 US-09-960-352-3400 12 US-10-051-952-4	17	99	1.9	640681	10	US-09-790-988-1	
12 US-10-051-952-4	c 18	55	1.8	446	10	US-09-960-352-3400	ന
	19	55	1.8	3876	12	US-10-051-952-4	Sequence 4, Appli

Sequence 4292, Ap Sequence 12872, A Sequence 12872, A Sequence 573, App Sequence 6528, App Sequence 5301, App Sequence 1221, App Sequence 1231, App Sequence 12911, A Sequence 12911, A Sequence 4090, App Sequence 301, App Sequence 5599, App Sequence 5599, App Sequence 5509, A	Sequence Just, Ap Sequence 11, Appl
US-09-878-574-4292 US-09-960-352-12872 US-09-960-352-573 US-09-891-641-40 US-09-960-352-6528 US-09-960-352-5301 US-09-960-352-583 US-09-960-352-583 US-09-960-352-583 US-09-960-352-1221 US-09-960-352-1221 US-09-960-352-1221 US-09-960-352-1221 US-09-960-352-1221 US-09-960-352-1221 US-09-960-352-1221 US-09-960-352-1221 US-09-960-352-14521 US-09-960-352-14521 US-09-960-352-1453 US-09-960-352-1453 US-09-960-352-1453 US-09-960-352-1453 US-09-960-352-1453 US-09-960-352-1453 US-09-960-352-1453 US-09-960-352-1453 US-09-960-352-1453 US-09-960-352-1453 US-09-960-352-1453 US-09-960-352-1453 US-09-960-352-1453 US-09-960-352-1453 US-09-960-352-1453 US-09-960-352-1453	US-09-960-352-508/ US-09-286-488-11
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519 428 428 1035 414 401 442 1437 2000 2000 2000 393 450 411 910 910 910 910 910 910 910 910 910 9	3/6 1287
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844444 4444 4444 4444 4444 4444 4444 4	47
22222222222222222222222222222222222222	44
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ALIGNMENTS

RESULT 1 US-09-879-959-9 ; Sequence 9, Application US/09879959 ; Patent No. US20020160489A1 ; GENERAL INFORMATION: ; APPLICANT: Weigel, Paul H ; APPLICANT: Kumari, Kshama ; APPLICANT: DeAncelis, Paul
; TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRES: ; TITLE OF INVENTION: IN BACILLUS SUBTILIS ; FILE REFERENCE: 3554.049 ; CURRENT APPLICATION NUMBER: US/09/879,959 ; CURRENT FILING DATE: 2001-09-12 ; PRIOR APPLICATION NUMBER: 09/469,200
; PKIOK FILING DATE: 1999-12-21 ; PRIOR APPLICATION NUMBER: 09/178,851 ; PRIOR FILING DATE: 1998-10-26 . WINDED OF CRO IN MOS. 10
; NOWHER OF SEC ID NOS: IO ; SCOTWARE: PatentIn version 3.1 ; SEQ ID NO 9 ; LENGTH: 2937
; TYPE: DNA ; ORGANISM: pasteurella multocida US-09-879-959-9
Query Match 76.6%; Score 2283.4; DB 9; Length 2937; Best Local Similarity 86.5%; Pred. No. 0;
vative 0
Qy 43 ATTTTAAAGGAAAGAAATGAATACATTATCACAAGCAATAAAAGCATATAACAGCAAT 102
Db 1 ATTTTTAAGGACAGAAAATGAATACATTATCACAAGCATAAAAAGCATATAACAGCAAT 60
Qy 103 GACTATGAATTAGCACTCAAATTATTGAGAAGTCTGCTGAAACCTACGGGGGAAAAATC 162
Db 61 GACTATCAATTAGCACTCAAATTATTTGAAAGTCGGCGGAAATCTATGGACGGAAAATT 120
Qy 163 GTTGAATTCCAAATGTAAAGAAAAACTCTCGACCAATTC 209
Db 121 GTTGAATTTCAAATTACCAAGAAAAACTCTCAGCACATCCTTCTGTAATTCA 180
Qy 210TTATGTAAGTGAAGATAAAAAAAAGGTGTTTGCGATAGCTCATTAGATATC 261

.	62 GCAACACCTCTTACTTTCCAACGTAAAAAATTAACTCTATCCGAATCAGAAAAAAC 321 	22 agtitaaaaaataaatggaaatctatcactgggaaaaatcggagaacgcagaaatcaga 381 	82 AAGGTGGAACTAGTACCCAAAGATTTTCCTAAAGATCTTGTTCTTGCTCCATTGCCAGAT 441 	42 CATGITAATGATITIACATGGTACAAAAATGGAAAAAAGCITAGGIATAAAGCCIGTA 501 	02 AATAAGAATATCGGTCTTTCTATTATTCCTACATTTAATCGTAGCCGTATTTTAGAT 561 	62 ATAACGTTAGCCTGTTTGGTCAATCAGAAACTAACTACCCATTTGAAGTCGTTGTTGCA 621 	22 GATGATGGTAGTAAGGAAAGTTACCATTGTGCAAAAATACGAACAAAAACTTGAC 681 	82 ATAAAGTATGTAAGACAAAAAGATTATGGATACAATTGTGTGCAGTCAGAAACTTAGGT 741 -	42 TTACGTACAGCAAAGTATGATTTTGTCTCGATTCTAGACTGCGGATATGGCACCACAACAA 801 	02 ITATGGGTTCATTCTTACTTACAGAACTATTAGAACACAATGATGTTTTAATTGGA 861 	162 CCTAGAAAATATGTGGATACTCATAATATTACGGCAGAACAATTCCTTAACGATCCATAT 921)22 TTAATAGAATCACTACCAAACCGCTACAAATAACAATCCTTCGATTACATCAAAAGGA 981 	982 AATATATCGTTGGATTGGAGATTAGAACATTTCAAAAAACGGATAATCTACGTCTATGT 1041 	942 GATTCTCCGTTTTCGTTGTTGCGGGTAATGTTGCATTTTCTAAAGAATGGCTAAAT 1101 	102 AAAGTAGGTTGGATGAAGAATTTAATCATTGGGGGGGGGG	162 TACAGATTATTTGCCAAAGGCTGTTTTTTCAGAGTAATTGACGGCGGAATGGCCATCCAT	222 CAAGAACCACCTGGTAAAGAAAATGAAACAGAACGCGAAGCTGGTAAAAGTATTACGCTT 1281 	282 AAAATTGTGAAAGGAAAGGTACCTTACATGGAAAGCTTTTACCAATAGAAGATTCA 1341
181 (322	382	442	502	562	622	682	742	, 802	86	92	96	7 1042	7 1102 5 1081	y 1162 5 1141	122	128
g	Qy Dp	Qy Db	Q D	oy G	QY Dp	9. Pb	QY Db	Q Pp	S S	O.Y	Qy Db	Qy Db	QQ Dp	Qy Gp	Qy Pp	Qy Db	Qy Db	Οy

2280 2340 2040 2100 2160 2241 2220 2301 2361 2421 2400 2061 2121 2181 2001 1980 1761 1881 1401 1461 1641 1701 GAAGAAATGGATAAGTTAAAAGATCTTAAACTCATTCAAAATAAAGATGCCAAAATGGCA AATGACATCTCATATACACGAGTAATAGACTAATAAAAACTGAGGCACATTTAAGTAAT GATATTATGAGAGAAAAGGTCCCTTATATCTATAGAAAACTTTTACCAATAGAAGATTCG **ACCACTAATAGAAACGTCAATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTGGCCA** ATTAGAGCTTGGCATTTAACGGATGGATTTAACGAAAATATTGAAAACGCCGTGGATTAT GACATGTTCCTTAAACTCAGTGAAGTTGGAAAATTTAAAACATCTTAATAAAATCTGCTAT CATITITGTIGIAGICAATCAGICAITAAAIAGACAAGGCAICAAITAITAIAAITAIGAC **AAATTTGATGATTTAGATGAAAGTAGAAAGTATATCTTCAATAAAACCGCTGAATATCAA** GAATTTTCACGAGAAAAACTCACAACGGCTATGATTGCTCACCATTTTAGAATGTTTACG CCTAGGGTACGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCC TGTAACGATGGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAAT GTTTCTTTTGCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCT 2182 2302 1822 1882 1861 1942 1921 2002 1981 2062 2041 2122 2161 2242 2221 2281 2362 1702 1681 1762 1741 1801 2101 2341 1381 1582 1561 1261 1342 1321 1402 1462 1522 1501 qq 셤 q Ω QQ δ qq Dp QQ g Qγ δy QΥ QΥ δy Dp qq δλ g δy g Qγ qq QΥ g ò QQ QΥ Db δŽ g g δŽ Ω ŏ δ

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APPLICANT: Miyake, Katsuhide
APPLICANT: Matanabe, Masaki
APPLICANT: Matanabe, Masaki
APPLICANT: Iijima, Shinji
TITLE OF INVENTION: Beta 1,3-galactosyltransferase and DNA encoding the same
FILE REFERENCE: 766.53
CURRENT APPLICATION UNMBER: US/09/900,038A
CURRENT APPLICATION NUMBER: JP 2001-09-21
PRIOR APPLICATION NUMBER: JP 2001-392
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1414 GTAGATAGTGCTCTTAATCAAACTGTTGTTGGATCTCGAGGTTTGTATTTGTAACGATGGT 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGC 1533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1001 ATGCCCAAAATTAGTATTATTGTTCTGTATACAATGTAGAAAAATATTAGAAAAATGT 1060
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                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                        Length 5550;
                                                                                                                                                                                                                                                                                        2.9%; Score 86; DB 10; Length 55
54.0%; Pred. No. 6.8e-08;
tive 0; Mismatches 150; Indels
                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 137:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptococcus agalactiae type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1301 CTATTATATACAATATCGTAAAGA 1326
                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 137:
  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3, Application US/09900038A
; Patent No. US20020142425A1
; GENERAL INFORMATION:
                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 5550 base pairs
                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                               Best Local Similarity 54.0°
Matches 176; Conservative
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CDS
(2843)..(3979)
CDS
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LOCATION: (
NAME/KEY: C
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LENGTH: 68
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                        2641 CAAGGTATGTTTATGACGTATGCGCTAGCGCATGAGCGTCTCTGACGATTATAAAGAAGTC 2700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2821 CTGACTTATATGCCTTGGGAACGAAAATTACAATGGACAAAATGAACAAATTGAAAGTGCA 2880
                                                                                                                                                                           TICTCAGCATTAACACATGATTGGATCGAGAAAATCAATGCGCATCCACCATTAAAAAG 2601
                                                                                                                                                                                                                       2521 TTCTCAGCATTAACACATGATTGGATCGAGAAAATCAATGCGCATCCACCATTTAAAAAG 2580
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                                                                                                                                                                                                                                                                 CTGATTAAAACCTATTTAATGACAATGACTTAAGAAGTATGAATGTGAAAGGGGCCATCA 2661
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                                                                                        AGCCTATTCGTTAAAAATGACAGCTATGCTTATATGAAAAAATATGATGTCGGCATGAAT
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM, MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION UMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. HOOVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 137, Application US/09070927A Patent No. US20020120116A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION DATA:
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ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-070-927A-137
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NAME/KEY: CDS
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US-09-870-759-83
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Sequence 1, Application US/09816028A

Patent No. US20020042369A1

GENERAL INFORMATION:

APPLICANT: Gilbert, Michel

APPLICANT: Makarchuk, Warren W.

APPLICANT: National Research Council of Canada

TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of

TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of

TITLE OF INVENTION: Canadias and Ganglioside Mimics

FILE REFERENCE: 019633-0001110S

CURRENT APPLICATION NUMBER: US 80/9/816,028A

CURRENT PILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/118,213

PRIOR APPLICATION NUMBER: US 60/118,213

PRIOR PREDICATION NUMBER: US 09/495,406

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 49

SOSTWARER PATENTING DATE: 2000-01-31

SOSTWARER PATENTING NOS: 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1356 ACCTTTAGTTTCTATTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGT 1415
                                                                                                                                                                                                                                                                                                                                                                                       CTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTTGCTAAAGGTT 1600
                                                                                                                                                                                                                                                                            4058 CCGTCCTACAACAGACTCATTCATTGATAGAAGTTATACTGATTAATGATGGATCCACTG 4117
                                                                                                                                                                                                                                                                                                                                                    4118 ATAATAGTGGAGAAATTTGTGATAATTTATCTCAAAAAGACGATCGCATACTTGTATTTC 4177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1361 TAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGTAGATA 1420
                                                                                                                                                                                                  3998 TTGTTTCTATCGTTATACCTATATACAACTCGGAAGCATATCTTAAAGAATGCGTGCAAT 4057
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0
                                                                                       Length 6865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384; OTHER INFORMATION: including LOS blosynthesis locus US-09-816-028A-1
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                                                                                                                            Indels
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Best Local Similarity 51.2%; Pred. No. 1.7e-06;
Matches 211; Conservative 0; Mismatches 198;
                                                                                       DB 10;
                                                                                     Score 80.6; DB 10;
Pred. No. 8.1e-07;
0; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4298 TAAAAATTTAATCACTGA 4316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1661 TAAAAGAATTTTTAAAAGA 1679
                                                                                         2.7%;
                                                                                                                              Conservative
                         ; LOCATION: (5009)..(5947)
US-09-900-038A-3
 (3982)..(4953)
                                                                                                          Best Local Similarity
Matches 170; Conserva
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US-09-816-028A-1/c
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LOCATION:
NAME/KEY:
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APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT APPLICATION NUMBER: US 60/208,128
PRIOR PILLING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 83
LENGTH: 17276
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1416 AGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTC 1475
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                                                                                                              AACAGATAATACCTTAGAAGTGATCAATAAGCTTTTATGGTAATAATCCTAGGGTACGCAT
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Pred. No. 1.8e-05;
0; Mismatches 213;
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Best Local Similarity 48.7%;
Matches 202; Conservative (
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; OTHER INFORMATION:
US-09-870-759-83
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us-09-842-484a-1.rnpb

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RESULT 8
US-09-816-028A-30
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                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                           Sequence 9, Application US/09767041
Fatent No. US20020055168A1
GENERAL INFORMATION:
FALENT Smith, Hida
TITLE OF INVENTION:
STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS
FILE REPRENCE:
2 183-4726
CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
FRIOR FILING DATE: 1999-07-19
FRIOR FILING DATE: 1998-07-22
FRIOR PLIANG DATE: 1998-07-22
FRIOR PLIANG DATE: 1998-07-22
FRIOR FILING DATE: 1998-07-22
FRIOR PLIANG DATE: 1998-07-22
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1632 TCTTGAGCCTGATGCAGTTGAACTGTGTTTAAAAGAATTTTTAAAAGATAAAACG 1686
                                 9502 AGTITCCTCTGATTACATAGCGAATTIGTATAATGCTATTCAAAAACATGATTCG 9556
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Pred. No. 2.2e-05;
0; Mismatches 203;
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GENERAL INFORMATION: APPLICANT: Smith, Hilda
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Best Local Similarity 49.0%;
Matches 195; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Streptococcus suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature; LOGATION: (1)..(6992); COTHER INFORMATION: CPS 2 US-09-767-041-9
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                                                                                                                        RESULT 6
US-09-767-041-9
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Sequence 30, Application US/09816028A

Fatent No. US20020042369A1

GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wational Research Council of Canada
TITLE OF INVENTION: CamplyLobacter Glycosyltransferases for Blosynthesis of
TITLE OF INVENTION: Camplosides and Ganglioside Mimics
TITLE OF INVENTION: Canadias: US/09/816,028A
CURRENT FILING DATE: 2001-03-21

FRIOR FILING DATE: 1999-02-01

FRIOR FILING DATE: 1999-02-01

FRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 49

SOFTWARE: Patentin Ver. 2.1
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      STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS
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TITLE OF INVENTION: STREPTOCOCCUS SUIS VAC
FILE REFERENCE: 2183-4726
CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1998-07-19
PRIOR FILING DATE: 1998-07-22
PRIOR APPLICATION NUMBER: EP98202465.5
PRIOR APPLICATION NUMBER: EP98202465.1
PRIOR APPLICATION NUMBER: EP98202467.1
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 53
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Pred. No. 2.
                                                                                                                     PCT/NL99/00460
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Best Local Similarity 49.0°
Matches 195; Conservative
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CTHER INFORMATION: CPS1
US-09-767-041-29
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TYPE: DNA
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APPLICANT: Gilbert, Michel
APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wational Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFERENCE: 019633-0001110S
CURRENT APPLICATION NUMBER: US/09/816,028A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-01-01
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LOCATION: (1)..(912)

OTHER INFORMATION: Campylobacter glycosyltransferase B (CgtB) beta-1,3

OTHER INFORMATION: galactosyltransferase from C. jejuni serotype 0:2

OTHER INFORMATION: (strain NCTC 11168)

US-09-816-028A-28
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                                                                                                                                                                                                                                                                                                                                                                                                  1482 TAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGCATCATGTC 1541
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                                                                                                                                                                                                                                                    1362 AGTITICTATITATATICCCCGCTTATAACTGTGCAAATTATATICAAAGATGTGTGTAGATAG 1421
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                                                                                                                                                                                                                                                                                                                                                              69 TIGTATCAATCAGACTITTAAAAATATAGAAATAATTGTAGTTGATGATTGTGGAAGTGA 128
                                                                                                       COTHER INFORMATION: beta-1,3 galactosyl transferase from C. jejuni 0:10 US-09-816-028A-30
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ilarity 53.2%; Pred. No. 0.0002;
Conservative 0; Mismatches 143;
                                                                                                                                                                          Score 68.4; DB 10;
Pred. No. 0.00011;
0; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTAAAAGAATTTTTAAAAGATAAAA 1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATGAAAATTTTAAAAAACAATGAAA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/09816028A Patent No. US20020042369A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Campylobacter jejuni
                                  TYPE: DNA ORGANISM: Campylobacter jejuni
                                                                                                                                                                              Query Match 2.3%;
Best Local Similarity 52.8%;
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 912
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Matches 166;
                                                                                        NAME/KEY: CDS
SEQ ID NO 30
LENGTH: 891
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1987 ATTCAAAAGAAAAACCATTTTGTTGTAGTCAATCAGTCATTAAATAGACAAGGCATCAAT 2046
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                                                                                                                                                                                                                                                                                                                                      .542 TA---AACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCGTTTCTTTTGCTAAAGG 1598
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1362 AGTITCTATITATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGTAGATAG 1421
                                                                                                                                                                                                                                                                                  249 ACCITATATCTTTTTAGATTCTGATGATTATTTAGACTTAATGCTTGCGAAGAATG 308
                                                         9 AATITICCATCATACTACCAACTTATAATGTGGAAAAATATATTGCTAGAGCATTAGAAAG
                                                                                                                                                                 69 TIGCATTAACCAAACITTTAAAGATATAGAAATCATTGTAGTAGATGATTGTGGTAATGA
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45.8%; Pred. No. 0.00028;
tive 0; Mismatches 317;
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Sequence 1, Application US/09351794A
Sequenct No. US20020042382A1
GENERAL INFORMATION:
APPLICANT: DUFFY, PATRICK E.
APPLICANT: OCKENHOUSE, CHRISTIAN F.
TITLE OF INVENTION: SEQUESTRIN
FILE REPRENCE: 38644-175519
CURRENT APPLICATION NUMBER: US/09/351,794A
CURRENT FILING DATE: 1999-07-13
PRIOR APPLICATION NUMBER: 08/559,896
PRIOR FILING DATE: 1995-11-17
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
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US-09-351-794A-1
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us-09-842-484a-1.rnpb

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Query Match
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Patent No. US20020042369A1

GENERAL INRORAMION:

APPLICANT: Gilbert, Michel

APPLICANT: Wational Research Council of Canada

TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of

TITLE OF INVENTION: Ganqliosides and Ganglioside Mimics

FILE REFERENCE: 019633-0001110s

CURRENT APPLICATION NUMBER: US/09/816,028A

CURRENT APPLICATION NUMBER: US 60/118,213

PRIOR FILING DATE: 1999-02-01

PRIOR APPLICATION NUMBER: US 09/495,406

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PATENT VET. 2000-01-31

SEQ ID NO 26

LENGTH: 906
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OTHER INFORMATION: beta-1,3-galactosyltransferase from C. jejuni strain
OTHER INFORMATION: OH4384 (ORF 6a of lipooligosaccharide (LOS)
OTHER INFORMATION: biosynthesis locus)
                                            AATATTTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTAATAAAAAACTGAG 2406
                                                                                                                                                             1422 TGCTCTTAATCAAACTGTTGTCGATCTTCGAGGTTTGTATTTGTAACGATGGTTCAACAGA 1481
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1528 AAAAATATTCAGATTATTCAAGAGGATAATATAAAAAATAAAGGCCAAAAGGATAACACT 1587
                                                                                                                                 2407 GCACATITIAAGTAATATTAAATTAAGTCAGTTAAATCTAAATTGTGAATACATCATT 2466
                                                                                                                                                                                                                           2467 TTTGATAATCATGACAGCCTATTCGTTAAAAATGACAGCTATGCTTATATGAAAAAATAT 2526
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                                                                                       1588 GAAATGTTAGATAATAATGAAAGGAAATA----ACAAATATTGATATAAAAAATGTTGAT 1641
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                                                                                                                                                                                                                                                                                                                                                     GTTGATGGTATAAACAATGTGGGAGATATAAACAATGCTGGAGATACAAATAATGC 1817
                                                                                                                                                                                                                                                                                                                    2527 GATGTCGGCATGAATTTCTCAGCATTAACACATGATTGGATCGAGAAAATCAATGC 2582
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51.3%; Pred. No. 0.00026;
live 0; Mismatches 169;
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US-09-816-028A-26
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Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
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1659 TITAAAAGAATITITAAAAGATAAAACGCTAGCTIGTGTTTATACCACTAATA 1711
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                               309 TATAAAAATTTTAGATGAACAGGATGAAGTTGATTTAGTGTTTTTCAATGCTA 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diskette, 3.50 inch, 1.4Mb storage
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Pred. No. 0.0028;
1; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <URKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; SEQUENCE DESCRIPTION: SEQ ID NO: 308.
US-09-070-927A-308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                     Sequence 308, Application US/09070927A Patent No. US20020120116A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 308:
                                                                                                                                                                                                                                                    APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2406 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII TEXT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
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Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                             US-09-070-927A-308/c
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Matches 207;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1471 GGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTA 1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1531 CGCATCATGTCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTT 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1411 TGTGTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGAT 1470
2131 TGGGGGAATTGGAAAAGCCTTTAACTTGGGTGTTTCAGAAGCAAAAGGTGATATTGC 2072
                                                                                                                                                                                                                   APPLICANT: Choi et. al. TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 GAAACTCTATATAAAAAATAGTAGAGTATCAGGCTGATATTGCAGTTGGTAATTATTAT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 GGTTCTACGGATGCTTCAGGTGAAATTTGTAAAGAATTTTCAGAAATGGATCACCGAATT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TGCCTAGATAGTATTATTACTCAAACATATAAAAATATTGAGATTGTTGTCGTTAATGAT
                                                             2071 TGAATITGAAAGTGACGAITATGTAGCAITGCAIGCCIAIGACGIITAIACAA 2018
                                   1611 GCAGTTAGATTCAGATGATTATCTTGAGCCTGATGCAGTTGAACTGTGTTAAA 1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2023;
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Pred. No. 0.0046;
0; Mismatches 294; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                        Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQUENCE DESCRIPTION: SEQ ID NO: 199: US-09-765-272-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MSDOS version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Scier
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                              Sequence 199, Application US/09765272 Patent No. US20020061545A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                          STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        best Local Similarity Matches 237; Conserva
                                                                                                                                  RESULT 13
US-09-765-272-199
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APPLICANT: Warner, Wesley C.
APPLICANT: Warner, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Magappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37.21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
OURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2085 TAGAAAGTATATCTTCAATAAAACCGCTGAATATCAAGAAGAAATGGATATGTTAAAAGA 2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2025 ATTAAATAGACAAGGCATCAATTATTATAATTATGACAAATTTGATGATTTAGATGAAAG 2084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1711 AGAAACGICAATCCGGAIGGIAGCITAATCGCIAAIGGITACAAITGGCCAGAAITITCA 1770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 TCTTTCAACGAAAGTGAAGGAATGTTCTACTTTCATATATTGGGAGACTCCTATTATGAG
                                                                                          CGAGAAAAACTCACAACGGCTATGATTGCTCACCATTTTAGAATGTTTACGATTAGAGCT
                                                                                                                                                                                     1831 TGGCATTTAACGGATGGATTTAACGAAAATATTGAAAACGCCGTGGATTATGACATGTTC
                                                                                                                                     362 AAAGTATATGATAATGTTTCTATCTTTGAGAACTTGTATGAAACTCAAGAAATGAAGAGT
                                                                                                                                                                                                                                422 TTTGCTTTGATATCTGCTTGGGGTAAACTCTATAAGGCAAGATTGTTTGAGCAGTTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 516;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure

: LOCATION: (76).(90)

OTHER INFORMATION: unsure at all n locations

: OTHER INFORMATION: Clone ID: 25-LIB3057-018-Q1-K1-G1

US-09-960-352-5785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58.8; DB 10;
Pred. No. 0.0073;
0; Mismatches 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                     US/09960352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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Sequence 5558, Application US/09960352

Sequence 5558, Application US/09960352

Patent No. US20020137139a1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengbing

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: US/09/980, 352

CURRENT APPLICATION NUMBER: US/09/960, 352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 13112

SEQ ID NO 5558

LENGTH: 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2284 AAGAATCATCTTACACCAGACATCAAAAAAAAAATATTGGCTTTCTATCATAAGCACCAA 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2104 AAAACCGCTGAATATCAAGAAGAAATGGATATGTTAAAAGATCTTAAACTCATTCAAAAT 2163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2224 AAACTAAACAATATTATTGAATATAAAAAATATATTCGTTATTATTATTGTTGAT 2283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2344 GTGAATATTTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTAATAAAAACT 2403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2404 GAGGCACATITAAGTAATATAATAAATTAAGTCAGTTAAATCTAAATTGTGAATACATC 2463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.0%; Score 58.6; DB 10; Length 431; llarity 47.6%; Pred. No. 0.0076; Conservative 0; Mismatches 189; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INCEMATION: Clone ID: 24-LIB3057-024-Q1-K1-F7
US-09-960-352-5558
                                                           2445 TCTAAATTGTGAATACATCATTTTTGATAATCATGA 2480
                                                                                        94 ATATNAAAACTAACCCTCNATACCTTATTGCCATTA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: January 4, 2003, 02:22:36
Job time : 277 secs
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Best Local Similarity
Matches 172; Conserva
                                                                                                                                                                   RESULT 15
US-09-960-352-5558/c
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                                                                     ; Search time 5768 Seconds
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/cgn2_6/ptodata/1/pna/US098C_COMB.seq:*
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Ptodata/1/pna/US100A_COMB.seq:*
ptodata/1/pna/US100B_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US102B_COMB.seqi
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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60: /cgn2_6/ptodata1/pna/
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1, Appli			Sequence 8, Appl1	Sequence 8, Appl1	Sequence 2, Appli	Sequence 2, Appl1	Sequence 2, Appl1	Sequence 9, Appl1	Sequence 9, Appli	Sequence 2, Appli	Sequence 2527, Ap	Sequence 2527, Ap	Sequence 2987, Ap	Sequence 137, App	Sequence 137, App		Sequence 2421, Ap	Sequence 3, Appl1	Sequence 1938, Ap	Sequence 1, Appli
QI	PCT-US01-1335-1	PCT-US99-2657 -4	PCT-US01-13395-3	US-10-011-768B-8	US-10-011-771B-8	PCT-US99-07289-2	US-09-283-402-2	US-09-469-200-2	0-656-618-60-SD	US-10-172-527-9	PCT-US99-26501-2	US-09-107-532-2527	US-09-107-532A-2527	US-09-134-000-2987	US-09-070-927-137	US-09-070-927A-137	US-09-666-355A-6574	US-10-015-127-2421	US-09-900-038A-3	US-10-015-127-1938	US-09-495-406-1
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GENERAL INFORMATION:
APPLICANT: THE BOARD OF RECENTS OF THE UNIVERSITY OF OKLAHOMA
TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
FILE REFERENCE: 617481-5
CURRENT APPLICATION NUMBER: PCT/US99/26501
CURRENT APPLICATION NUMBER: 60/107,929
EARLIER APPLICATION NUMBER: 60/107,929
EARLIER FILING DATE: 1999-11-11
EARLIER FILING DATE: 1999-04-01
SEARLIER FILING DATE: 1999-04-01
SOFTWARE: Patentin Ver. 2.0
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çy Dp	421	GTTCTTGCTCCATTGCCAGATCATGTTAAATGATTTTACATGGTACAAAAATCGAAAAAA 480
oy Db	481	AGCTTAGGTATAAAGCCTGTAAATAAGAATATCGGTCTTTCTATTATTCTTATTCCTACATTT 540
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Q Db	721	TGTGCAGTCAGAAACTTAGGTTTACGTACAGCAAAGTATGATTTTGTCTCGATTCTAGAC 780
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Qy Db	1021 1021	ACCGATAATCTACGTCTATGTGATTCTCCGTTTCGTTATTTTGTTGCGGGTAATGTTGCA 1080
Qy	1081	TTTTCTAAAGAATGGCTAAATAAAGTAGGTTGGTTGGAGAAGAATTTAATCATTGGGGG 1140
Qy Db	1141	GGCGAAGATGTAGATTTGGTTACAGATTATTTGCCAAAGGCTGTTTTTTCAGAGTAATT 1200
Qy Dp	1201	. GACGGCGGAATGGCCATCCATCAAGAACCACCTGGTAAAGAAAATGAAACAGAACGCGAA 1260

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                                                                      AAATATGATGTCGGCATGAATTTCTCAGCATTAACACATGATTGGATCGAGAAATCAAT
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GENERAL INPORMATION:
TERRETAIN BE ANGELIS, PAUL L.
TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE
TITLE OF INVENTION: USING SAME
TITLE OF INVENTION: USING SAME
TITLE OF INVENTION: USING SAME
CURRENT APPLICATION NUMBER: PCT/US01/13395
CURRENT FILING DATE: 2001-04-25
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
SOFTWARE: PATENTIN VOYER: 3
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Best Local Simi
Matches 2969;
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           AAATTATTTGAGAAGTCTGCTGAAACCTACGGGCGAAAAATCGTTGAATTCCAAATTATC
                                                    AAATGTAAAGAAAACTCTCGACCAATTCTTATGTAAGTGAAGATAAAAAAACAGTGTT
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1141 GGCGAAGATGTAGAATTTGGTTACAGATTATTTGCCAAAGGCTGTTTTTTCAGAGTAATT	1261 GCTGGTAAAAGTATTACGCTTAAAATTGTGAAAAAGGGTACCTTACATCTATAGAAAG 1320 1261 GCTGGTAAAAGTATTACGCTTAAAATTGTGAAAGAAAAGGTACCTTACATCTATAGAAAG 1320 1321 CTTTTACCAATAGAAGTTCACATATTCATAGAATACCTTTAGTTTATTATTATACCC 1380		GTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACAGATAATACCTTAGAAGTGATC 1 	01 AATAAGCTTTATGGTAATAATCCTAGGGTACGCATCATGTCTAAACCAAATGGCGGAATA 1	1561 GCCTCAGCATCAAATGCAGCCGTTTCTTTGCTAAAGGTTATTACATTGGGCAGTTAGAT 1620 	1621 TCAGATGATTATCTTGAGCCTGATGCAGTTGAACTGTGTTTAAAAGAATTTTAAAAGAT 1680 	1681 AAAACGCTAGCTTGTGTTTATACCACTAATAGAAACGTCAATCCGGATGGTAGCTTAATC 1740 	1741 GCTAATGGTTACAATTGGCCAGAATTTTCACGAGAAAACTCACAACGGCTATGATTGCT 1800 	1801 CACCATTTTAGAATGTTTACGATTAGAGCTTGGCATTTAACGGATGGAT	1861 ATTGAAACGCCGTGGATTATGACATGTTCCTTAAACTCAGTGAAGTTGGAAATTTAAA 1920 	1921 CATCTTAATAAATCTGCTATAACCGCGTATTACATGGTGATAACACATCCATTAAGAAA 1980 	1981 CTCGGCATTCAAAAGAAAACCATTTGTTGTTGTCCAATCAGTCATTAAATAGACAAGGC 2040 	2041 ATCAATTATTATAATTATGACAAATTTGATGATTTAGATGAAAGTAGAAAGTATATCTTC 2100 	2101 AATAAAACGGCTGAATATCAAGAAATGGATATGTTAAAAGATCTTAAACTCATTCAA 2160 	2161 AATAAAGATGCCAAAATGGCAGTCAGTATTTTCTATCCCAATACATTAAACGGCTTAGTG 2220 	2221 AAAAAACTAAACAATATTGAATATAAAAAAATATATTCGTTATTGTACTTGTT 2280
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                                 GATAAGAATCATCTTACACCAGACATCAAAAAAGAAATATTGGCTTTCTATCATAAGCAC
                                                                                         worth (www. gruence 8) Application US/10011768B
WEREL INFORMATION:
PPLICANT: Weigel, Paul H.
PPLICANT: DeAngelis, Paul
PPLICANT: DeAngelis, Paul
TILE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof
ILE REPERENCE: 3554.011
URRENT PPLICATION NUMBER: US/10/011,768B
RIOR FILING DATE: 2001-12-11
RIOR APPLICATION NUMBER: US 09/178,851
RIOR PLILING DATE: 1998-10-26
RIOR FILING DATE: 1997-10-31
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Score 2285; DB 38;
Pred. No. 0;
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CCTAGGGTACGCATCATGTCTAAACCAAATGGGGGAATAGCCTCAGCATCAAATGCGCCCCAGCCCCCAGCATCAAATGCAGCCCCCAGCATCAAATGCAGCACCAGCATCAAATGCCAGCAATAGCCTAGCATCAAATGCAGCATCAAATGCCAGCATCAAATGCAGCATCAAATGCAGCATCAAATGCAGCATCAAATGCAGCATCAAATGCAGCATCAAATGCAGCATCAAATGCAGCATCAAATGCAGCATCAAATGCAGCATCAAATGCAGCACCAGCATCAAATGCAGCA GAATTTTCACGAGAAAAACTCACACAACGGCTATGATTGCTCACCATTTTAGAATGTTTACG CATATTCATAGAATACCTTTAGTTTCTATTTATATCCCCCCTTATAACTGTGCAAATTAT ATTCAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATT TGTAACGATGGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAAT ATTAGAGCTTGGCATTTAACGGATGGATTTAACGAAAATATTGAAAACGCCGTGGATTAT GATTCTCCGTTTCGTTATTTTGTTGCGGGTAATGTTGCATTTTCTAAAGAATGCTAAAT **AAAATTGTGAAAGAAAGGTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCA AAAGTAGGTTGGTTCGATGAAGAATTTAATCATTGGGGGGGCGGAAGATGTAGAATTTGGT** Db g q q q δ g QQ 9 ò qq ò g ò QQ ò g δ à g δy δ ò qq ò qq ŏ q οy g ò q ò ò ò

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TYPE: DNA
ORGANISM: Pastuerella Multocida
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SOFTWARE: P
SEQ ID NO 8
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APPLICANT: DeAngelis, Paul
APPLICANT: Kumari, Kshana
TITLE OF INVENTION: Hyaluronan Synthase Ger
FILE REFERENCE: 3554.011
CURRENT APPLICATION NUMBER: US/10/011,771B
CURRENT FILING DATE: 2001-10-11
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US-10-011-771B-8
Sequence 8, Application US/10011771B
SEGREAL INFORMATION:
APPLICANT: Weigel, Paul H.
APPLICANT: DeAngelis, Paul
APPLICANT: Kumari, Kshama
TITLE OF INVERTION: Hyaluronan Synthase
TILE REFERENCE: 3554.011
CURRENT APPLICATION UMBER: US/10/011,
CURRENT FILING DATE: 1998-10-26
FRIOR FILING DATE: 1998-10-26
FRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 10
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CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: US 09/178,851
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: US 60/064,435
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 10

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Length 2937;
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DB 38;
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Score 2285;
         Pred. No.
Query Match 76.7%;
Best Local Similarity 86.5%;
Matches 2541; Conservative
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Sequence 2, Application PC/TUS9907289
GENERAL INFORMATION:
APPLICANT: Board of Regents of the University of Oklahoma
APPLICANT: Board of Regents of the University of Oklahoma
TITLE OF INVENTION: NUCLEIC ACID ENCODING HYALURONAN SYNTHASE AND METHODS
TITLE OF INVENTION: OF USE
FILE REFERENCE: 617022-7
CURRENT APPLICATION NUMBER: PCT/US99/07289
CURRENT FILING DATE: 1999-04-01
EARLIER APPLICATION NUMBER: 60/080,414
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                                                                                      Score 2283.4;
Pred. No. 0;
                                                                                                      0; Mismatches
EARLIER FILING DATE: 1998-04-02
EARLIER APPLICATION NUMBER: 60/178,851
EARLIER FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
                                                                multocida
                                                                                      76.6%;
llarity 86.5%;
Conservative
                                                                Pasteurella
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                       CCAAGAAAATACATCGATACACAACATATTGACCCAAAAAGACTTCTTAAATAACGCGAGT
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FILE REFERENCE: 5820.530
CURRENT APPLICATION NUMBER: US/09/283,402
CURRENT FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 2937
TYPE: DNA

multocida

Pasteurella

; ORGANISM: Pi US-09-283-402-2

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Sequence 2, Application US/09283402
GENERAL INFORMATION:
APPLICANT: Paul DeAngelis
TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA
TITLE OF INVENTION: MULTOCIDA AND USES THEREOF

US-09-283-402-2

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Score 2283.4;
Pred. No. 0;
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76.6%;
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Conservative
Query Match
Best Local Similarity
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δ	, a	ATATATCGTTGGAGATTAGAACATTTCAAAAAACCGATAATCTACGTCTAT	1041
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Qy Pb	1222	3AACCACCTGGTAAAGAAAATGAAAC 	1281
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δλ	1342	ATTCATAGAATACCTTT	4
Op	1321	CAATAGAGTACCTTTAGTTTCAATTTATATCCCAGCTTATAACTGTGCAAAC	38
ζ. qa	1402	CAAAGATGTGTAGATAG 	1461
δy	46	TGTAACGATGG:	1521
Op	4	TGTAACGATGGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAA	0 1
Qy Db	1522	CCTAGGGTACGCATCATGTCTAAACCAAATGGGGGAATAGCCTCAGCATCAAATGCAGCG	1581 1560
Qy	1582	GTTTCTTTGCTAAAGGTTATTACATTGGGC	164
QQ	1561	GTTTCTTTTGCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTT	162
Qy Db	1642	GATGCAGTTGAACTGTGTTTAAAAGAATTTT 	1701
Qy	1702	ACCACTAATAGAAACGTCAATCCGGATG	1761
Op	1681	ACCACTAATAGAAACGICAATCCGGAIGGIAGCTIAATCGCIAAIGGITACAAITGGCC	174
οy	1762	GAATTTCACGAGAAAACTCACAACGGCTATGATTGCTCACCATTTAGAATGTT	182
QQ	1741	GAATTITCACGAGAAAAACTCACAACGGCTATGATTGCTCACCACTTTAGAATGTTCA	180
Qy	1822	ATTAGAGCTTGGCATTTAACGGATGGATTTAACGAAAATATTGAAAACGCGTGGATTAT 	1881 1860
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Qy	1942	GGCGTATTACATGGTGATAACACATCCATTAAGAAACTCG	200
qa	1921	TGTATTACATGGTGATAACACATCAATTAAGAAACTTGGCATT	1980

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Regents of the University of Oklahoma
NUCLEIC ACID ENCODING HYALURONAN SYNTHASE AND METHODS
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US-09-469-200-2
Sequence 2, Application US/09469200
GENERAL INFORMATION:
APPLICANT: Board of Regents of the
TITLE OF INVENTION: NUCLEIC ACID EN
TITLE OF INVENTION: OF USE
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Pred. No. 0;
0; Mismatches
FILE REFERENCE: 617022-7
CURRENT APPLICATION NUMBER: US/09/469,200
CURRENT FILING DATE: 1999-112-21
PRIOR APPLICATION NUMBER: 60/080,414
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/178,851
PRIOR FILING DATE: 1998-10-26
NUMBER OF SED ID NOS: 29
SOFTWARE: PATENTIN Ver: 2.0
SED ID NO 2
LINTH: 2937
                                                                                                          ; TYPE: DNA
; ORGANISM: Pasteurella multocida
US-09-469-200-2
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86.5%;
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Sequence 9, Application US/09879959

RESULT 9 US-09-879-959-9

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APPLICANT: Weigel, Paul H
APPLICANT: Weigel, Paul H
APPLICANT: Kumari, Kshama
APPLICANT: Nemari, Kshama
APPLICANT: Nemari, Kshama
APPLICANT: Nemari, Kshama
TITLE OF INVENTION: STREPTOCOCCUS EQUISIMILIS HYA
TITLE OF INVENTION: IN BACILLUS SUBTILIS
FILE REFERENCE: 3554.049
CURRENT APPLICATION NUMBER: US/09/879,959
CURRENT FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1998-10-26
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86.5%; Pred. No. 0;
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SOFTWARE: PatentIn version 3.1
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Matches 2540; Conservative
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                                                                                                                                             SEQ ID NO 9
                                                                                                                                                                 TYPE: DNA
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o do	862	CCTAGAAAATATGTGGATACTCATAATATTACCGCAGAACAATTCCTTAACGATCCATAT 921
ογ	7	98
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oy Ob	982	AATATATCGTTGGATTGGAGATTAGAACATTTCAAAAAACCGATAATCTACGTCTATGT 1041
9 %	1042	GATTCTCCGTTTCGTTATTTGTTGCGGGTAATGTTGCATTTTCTAAAGAATGGCTAAAT 1101
δ	1102	AAAGTAGGTTGGTTCGATGAAGAATTTAATCATTGGGGGGGG
qq	1081	AAATCCGGTTTCTTTGATGAGGAATTTAATCACTGGGGTGGAGAAGATGTGGAATTTGGA 1140
65 da	1162	TACAGATTATTTGCCAAAGGCTGTTTTTTCAGAGTAATTGACGGCGGAATGGCCATCCAT
ογ	1222	CAAGAACCACCTGGTAAAGAAAATGAAACAGAAGCTGGGTAAAAGTATTACGCTT 1281
g	1201	CAAGAGCCACCAGGTAAAGAAAATGAAACCGATCGTGAAGCGGGAAAAAATTACGCTC 1260
oy o	1282	AAAATTGTGAAAGAAAAGGTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCA 1341
οy	4	140
QQ	1321	CATATCAATAGACTACCTTTAGTTTCAATTTATATCCCAGCTTATAACTGTGCAAACTAT 1380
Oy Dp	1402	ATTCAAAGATGTGTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATT 1461
Ş ç	1462	TGTAACGATGGTTCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAAT 1521
3 8	, ,	1 1 20
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Š Š	1582	GTTTCTTTTGCTAAAGGTTATTACATTGGGCAGTTAGATTCAGATGATTATCTTGAGCCT 1641
ò	64	AGTTGAACTGTGTTTTAAAAGAATTTTTAAAAGATAAAAGGCTAGCCTTGTGTTTTAT 170
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ογ	1702	ACCACTAATAGAAACGTCAATCCGGATGGTAACTGTAATCGCTAATGGTTACAATTGGCCA 1761
g	1681	ACCACTAATAGAAACGTCAATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTGGCCA 1740
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٥'n	1822	ATTAGAGCTIGGCATTTAACGGATGGATTTAACGAAAATATTGAAAACGCCGTGGATTAT 1881

2160 2241 2220 2301 2280 2361 2421 2400 2481 2460 2541 2520 2580 2640 1980 2040 2100 2181 2601 2661 2700 2781 2760 2820 1941 2001 2061 2121 2721 2841 2901 AAAAAAGGGAAAATATCCCGTTAACAAGTTCATTATTAATAGTATAACGCTATAA 2958 GACATGTTCCTCAAACTCAGTGAAGTTGAAATTTAAACATCTTAATAAAATCTGCTAT 2062 AAATTTGATGATTTAGATGAAAGTAGAAAGTATATCTTCAATAAAACCGCTGAATATCAA GAAGAAATGGATATGTTAAAAGATCTTAAACTCATTCAAAATAAAGATGCCAAAATCGCA GTCAGTATTTTCTATCCCAATACATTAAACGGCTTAGTGAAAAAACTAAACAATATTATT ATTAATAAATTAAGTCAGTTAAATCTAAATTGTGAATACATCATTTTTGATAATCATGAC AGCCTATTCGTTAAAAATGACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAAT CAATTTGCACTTTTAATCTTAGAAAAGAAAACCGGCCATGTATTTAATAAAAACTGGACC CAATTTGCACTTTTAATCTTAGAAAAGAAAACCGGCCATGTATTTAATAAAACATCGACC CTGACTTATATGCCTTGGGAACGAAATTACAATGGACAAATGAACAAATTCAAAGTGCA GACATGTTCCTTAAACTCAGTGAAGTTGGAAAATTTAAACATCTTAATAAAATCTGCTAT AACCGCGTATTACATGGTGATAACACATCCATTAAGAAACTCGGCATTCAAAAGAAAAAC CATTITGTTGTTAGTCAGTCATTAAATAGACAAGGCATCAATTATTATATTATGAC 2902 2182 2281 2482 2461 2542 2701 1861 1942 1921 2002 1981 2122 2101 2161 2302 2422 2401 2521 2602 2581 2662 2641 2722 2782 2761 2821 1801 1882 Qy Db Qy Db Oy Dp g g g qq QQ g 셤 ά qq ò q ò qq ò g ٥y qq οy g οý q οy g ò ŏ ò δ δ ò ò

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Pred. No. 0;
0; Mismatches
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                                                           GENERAL INFORMATION:
APPLICANT: Weigel, Paul H
APPLICANT: Kumari, Kshama
APPLICANT: Beangels, Paul H
APPLICANT: Deangells, Paul
TILE OF INVENTION: HYALURONAN SYNTHASE GENE:
FILE REFERENCE: 3554.048
CURRENT APPLICATION NUMBER: US/10/172,527
CURRENT APPLICATION NUMBER: 60/297,788
PRIOR APPLICATION NUMBER: 60/297,784
PRIOR PILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VETSION 3:1
SEQ ID NO 9:
                                            Sequence 9, Application US/10172527 GENERAL INFORMATION:
                                                                                                                                                                                                                                                      ; ORGANISM: pasteurella multocida
US-10-172-527-9
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ilarity 86.5%;
Conservative
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Best Local Simi
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                                                                                                                                   AAAAAAGGCGAAAATATCCCCGTTAACAAGTTCATTATTAATAGTATAACGCTATAA 2958
                                                                                                                                                     AAATCTATCACTGGGAAAAATCGGAGAACGCAGAAATCAGAAAGGTGGAACTAGTACCC
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Sequence 2, Application PC/TUS9926501
Sequence 2, Application:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
FILE REFERENCE: 617481-5
CURRENT APPLICATION NUMBER: 60/107,929
EARLIER APPLICATION NUMBER: 60/107,929
EARLIER APPLICATION NUMBER: 60/107,929
EARLIER APPLICATION NUMBER: 09/283,402
EARLIER PILING DATE: 1999-11-11
EARLIER FILING DATE: 1999-04-01
SARVIER FILING DATE: 1999-04-01
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Pred. No. 2.9e-273;
0; Mismatches 348;
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Best Local Similarity 82.5%;
Matches 1743; Conservative
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GTCAATCAGAAACAAACTACCCATTTGAAGTCGTTGTTGCAGATGGTGGTAGGAAAAAACAAAACAAAAAAAA	GATTATAGCTGGATTCTAGGACTGCGATAGAGGATTAGGGGTTCATTCTTATAGGTTCATTCTTATAGGTTCATTCTTATAGGTTCATTCTTATAGGTTCATTCTTATAGGTTCATTCTTATAGGTTCATTCTTATAGGTTCATTCTTATAGGTTCATTCTTATAGGTTCATTCTTATAGGTTCATTATTAGGTTCATTATAGGTTCATTATAGGTTCATTATAGGTTCATTATAGGTTCATTAGGTTCATTAGGTTTAAGAAATTGTTATAGAGTTTAAGAATTAAGAATTAAGAATTAAGAATCATTAAGAATCATTAAGAATCATTAAGAATCATTAAGAATCATTAAGAATCATTAAGAATCATTAAGAATCATTAAGAATCATAATAGAATCATAACGATAGATTAATAGAATCACTAACGATCATATAATAGAATCACTAACGATAGAATCATAAAGAATCATAAAGAATCATAAAAGAATCATAAAGAATCATAAAAAATAGAATCATAAAAAAAA	GAAACCGCTACAAATAACAATCCTTCGATTACATCAAAAGGAAATATATCGTTGGATTGCTTGC	TTGTTGCGGGTAATGTTGCATTTCTAAAGAATGGCTAAATAAA	GGCTGTTTTTCAGAGTAATTGACGGCGGAATGGCCATCCAT	GTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCACATATTCATAGAATACCT	AGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGTTCAACA	TCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCGGTTTCTTTTGCTAAAGGT
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7308
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                 2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                780 CTCACAACGGCTATGATTGCTCACCATTTTAGAATGTTTACGATTAGAGCTTGGCATTTA 1839
                                                                                                                                                    2080 GAAAGTAGAAAGTATATCTTCAATAAAACCGCTGAATATCAAGAAGAAATGGATATGTTA 2139
                                                                          1960 GATAACACATCCATTAAGAAACTCGGCATTCAAAAGAAAAAACCATTTTGTTGTAGTCAAT
                                                                                                                                                                                                                                                                                                                                                                               AATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTGGCCAGAATTTTCACGAGAAAAA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532
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NERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
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REGISTRATION NUMBER: 40,489
REPERENCE/DOCKET NUMBER: GTC-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0855
FILING DATE: May 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/05157
FILING DATE: JULY 2, 1997
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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-107-532-2527
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US-09-107-532A-2527
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Best Local
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US-09-107-532A-527
Sequence 2527 Application US/09107532A
Sequence 2527 Application US/09107532A
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
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                                                                                                                                                                                                                                                                                                                         Length 984;
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                     Query Match 3.0%; Score 89.2; DB 15; Best Local Similarity 54.2%; Pred. No. 1.3e-06; Matches 181; Conservative 0; Mismatches 153;
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APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/01571
FILING DATE: July 2, 1997
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                   ORGANISM: Enterococcus faecium
                                                                                              TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                   LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1...984
INFORMATION FOR SEQ ID NO:
                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                         ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                            ; LOCATION:
US-09-107-532-2527
                                                                                                                                                                                                                      FEATURE:
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Sequence 2987, Application US/09134000A
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-005
CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
SEQ ID NOS: 6810
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54.0%; Pred. No. 5.3e-06;
ive 0; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.0%; Score by z; Stanilarity 54.2%; Pred. No. 1.3e-06; Similarity 6.2%; Pred. No. 1.3e-06; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1649 TTGAACTGTTTAAAAGAATTTTTAAAAGATAA 1682
INME: ATINICAL PARELLA Deneke
RECISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-507
INFORMATION FOR SEQ ID NO: 2527:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 ATGAAATTTTGTATGAGAATTTGAAAATTCATGA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...984
SEQUENCE DESCRIPTION: SEQ ID NO: 2527:
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                         TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
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US-09-134-000-2987
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Best Local Similarity 54.0
Matches 176; Conservative
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                                                                     1473
                                                                                                                                        1474 TCAACAGATAATACCTTAGAAGTGATCAATAAGCTTTATGGTAATAATCCTAGGGTACGC 1533
1354 ATACCTTTAGTTTCTATTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGT 1413
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                          139 TCTCCAGACAGTTCTGGAGCAATGTGTGATCAGTTTGCTGAACAAGATCAACGGGTAAAA 198
                                                                                                                                                                                                                                  GTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 137, Application US/09070927

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
APPLICANT: Steven C. Barash
TITLE OF INVENTION: Enterococcus faccialis Polynucleotides and
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 9410 Key West Avenue CITY: Rockville STATE: Marvine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927
FILING DATE: herewith
                                                                                                                                                                                                                                                                                                                                                        1654 CTGTGTTTAAAAGAATTTTTAAAAGA 1679
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TELECOMMUNICATION INFORMATION:
TELEFAN: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
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NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
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Matches 176; Conservative
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APPLICATION NUMBER:
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US-09-070-927-137
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                                                                              GTAGATAGTGCTCTTAATCAAACTGTTGTCGATCTCGAGGTTTGTATTTGTAACGATGGT
1354 ATACCTTTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGT
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1 ttataaactgattaaagaag......acatttgcattttattaaaa
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2: /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USO3_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

7: /¢gn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*
                            Ltd.
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen,
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US-10-216-289-1

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US-10-309-134-000C-2987

US-10-303-161-1

US-10-303-161-1

US-10-303-128-1

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US-10-303-128-1

US-10-303-128-1

US-10-24-45-27

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US-10-240-45-28

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US-10-240-45-28

US-10-303-161-30

US-10-303-161-30

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US-10-303-128-30

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Maximum Match 100%
Listing first 45 summaries
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Sequence 1. Application US/09842484A

Sequence 1. Application US/09842484A

GENERAL INFORMATION:

APPLICANT: DEANGELIS.

APPLICANT: DEANGELIS.

TILE FOF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND USING SAMI FILE REPERENCE: 4605.003

CURRENT APPLICATION NUMBER: US/09/842,484A

CURRENT FILING DATE: 2001-04-25

PRIOR FILING DATE: 2000-04-25

NUMBER: 06/199,538

PRIOR FILING DATE: 2000-04-25

NUMBER: OF SEQ ID NOS: 7

SOFTWARE: PALENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ATGAATACATTATCACAAGCAATAAAAGCATATAAACAGCAATGACTATGAATTAGCACTC 120
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US-10-240-485-162
US-10-303-161-28
US-10-303-118-28
US-10-303-118-28
US-10-303-118-28
US-10-303-128-28
US-10-303-161-26
US-10-303-162-26
US-10-303-18-26
US-10-303-18-26
US-10-303-18-26
US-10-303-18-26
US-10-257-166-18
US-10-257-166-18
US-10-257-166-13
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100.0%; Pred. No. 0;
ive 0; Mismatches
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       Best Local Similarity 100.
Matches 2979; Conservative
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Sequence 3, Application US/09842484A
Sequence 3, Application US/09842484A
GENERAL INFORMATION:
TITLE COFINYERIES, PAUL L.
TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF M.
CURRENT PELLIA DATE: 2001-04-25
PRIOR PELLOATION NUMBER: 60/199,538
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENTIN NOS: 7
SEQ ID NO 3
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Best Local Similarity 99.7%;
Matches 2969; Conservative
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APPLICANT: Wedigel, Paul H.
APPLICANT: Enderalis, Paul
APPLICANT: Rumari, Kshama
TITLE OF INVENTION: Hyaluronan Synthase Gene and
FILE REFERENCE: 3554.011
CURRENT APPLICATION NUMBER: US/09/469,200D
CURRENT APPLICATION NUMBER: US/09/469,200D
PRIOR PILING DATE: 1999-12-21
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
SOFTWARE: PALCATION NUMBER: US 60/064,435
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PALCATION NUMBER: OS 60/064,435
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Pred. No. 0;
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; GENERAL INFORMATION:
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US-09-469-200D-8
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Best Local Similarity 86.5%;
Matches 2541; Conservative (
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APPLICANT: WEIGEL, PAUL H
APPLICANT: KUMARI, KSHAMA
TITLE OF INVENTION: HYALURONAN SYNTHASES AND METHODS OF MAKING AND USING :
FILE REFERENCE: 35541.08
CURRENT APPLICATION NUMBER: US/10/309,560
CURRENT FILING DATE: 2002-12-03
PRIOR PELICATION NUMBER: 60/336,105
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PATENTIN VERSION 3.1
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Pred. No. 0;
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ORGANISM: Pasteurella multocida
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Best Local Similarity 86.5%;
Matches 2540; Conservative
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Pred. No. 0;
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: DEANGELIS, PAUL
TITLE OF INVENTION: DAM ENCODING HYALURO);
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 35541.081
CURRENT APPLICATION NUMBER: US/10/217,61:
CURRENT FILING DATE: 2002-08-12
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/080,414
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENT NOS: 9
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Oy 3. Db 3	40 AAATCTATC 01 AAATTGCTC	CIATCACTGGGAAAAAATCGGAGAACGCAGAAATCAGAAAGGTGGAACTAGTACCC 399 	• 0
Qy 4 Db 3	00 AAAC 61 AAAC	ATTITCCIAAAGAICITGITCITGCICCATIGCCAGAICAIGITAANGAITITACA 459 	a 0
Qy 4 Db 4	60 21	TGGTACAAAAATCGAAAAAAAGCTTAGGTATAAAGCCTGTAAATAAGAATATCGGTCTT 519 	6 0
Qy 5 Db 4	20	TCTATTATTATTCCTACATTTAATCGTAGCCGTATTTTAGATATAACGTTAGCCTGTTTG 579 	6 0
QY 5 Db 5	80 GT 	CAATCAGAAACAACTACCATTTGAAGTCGTTGTTGCAGATGATGGTAGTAAGGAA 639 	
Oy 6 Db 6	40 AAC 01 GAT	TTACTTACCATTGTGCAAAAATACGAACAAAAACTTGACATAAAGTATGTAAGACAA 699 	
Qy 7. Db 6	00	AAAGATTATGGATATCAATTGTGCAGTCAGAAACTTAAGGTTTAOGTACAGCAAAGTAT 759 	
Oy 7 Db 7	60	GATTITGICICGAITCIAGACTGCGATAIGGCACCACAACAATTAIGGGTICAITCITAI 819 	
2y 8 0b 7	20	PACAGAACTATTAGAAGACAATGATATGTTTTAATTGGACCTAGAAATATGTGGAT 879 	
2y 8 0b 8	80	ACTCATAATATTACCGCAGAACAATTCCTTAACGATCCATATTTAATAGAATCACTACCT 939	
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Oy 10 Db 9	000 AGATT 	ragaacatticaaaaaaccgataatctacgtctatgtgattctccgtttcgttat 105' 	
Oy 10 Db 10	060 TTTG 021 TTTG	GTTCGAT 111 CTTTGAT 108	119
Oy 1.1 Db 10	120 GAAG 081 GAGC	AAGAATTTAATCATTGGGGGGGGGGAAGATGTAGAATTTGGTTACAGATTATTTGCCAAA 1175 	79
r-4	80 G	TGGTAAA 123	33

2259 2220 2040 2139 2100 2199 2160 2019 1980 2079 1659 1680 1779 1899 1860 1479 CAGTCATTAAATAGACAAGGCATCAATTATTATAATTATGACAAATTTGATGATTTAGAT GAAAGTAGAAAGTATATCTTCAATAAAACCGCTGAATATCAAGAAGAAATGGATATGTTA 1501 TCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCGTTTCTTTTGCTAAAGGT CTCACAACGGCTATGATTGCTCACCATTTTAGAATGTTTACGATTAGAGCTTGGCATTTA ACGGATGGATTTAACGAAAATATTGAAAACGCCGTGGATTATGACATGTTCCTTAAACTC 1540 TCTAAACCAAATGGCGGAATAGCCTCAGCATCAAATGCAGCCGTTTCTTTTGCTAAAGGT TTAGTTTCTATTTATATCCCCGCTTATAACTGTGCAAATTATATTCAAAGATGTGTAGAT GTACCTTACATCTATAGAAAGCTTTTACCAATAGAAGATTCACATATTCATAGAATACCT GAAAATGAAACAGAACGCGAAGCTGGTAAAAGTATTACGCTTAAAAATTGTGAAAAAAG 1681 1801 2041 2140 2200 2260 1621 1720 1741 1840 1900 1960 1921 2020 1981 2080 2101 2161 1600 1561 1660 1861 1420 1381 1780 1141 1240 1201 1300 1261 1360 g qq δλ QY qq ŏ Dp QQ Db δy Q Q οy δy δ Qy g qq ŏλ g ò qq δý qq δy Db QY Db Qγ g Ωp ÓΥ òγ QΥ δ



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APPLICANT: SIGIURA, NOBUO
APPLICANT: SIGIURA, NOBUO
APPLICANT: KIMATA, KOJI
TITLE OF INVENTION: CHONDROITIN POLYMERASE AND DNA ENCODING THE SAME
FILE REFERENCE: 226882US0
CURRENT PAPLICATION NUMBER: US/10/216,289
CURRENT PILING DATE: 2002-11-04
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: JP 2001-324127
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-0-31
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                                                                         Sequence 3, Application US/10216289 GENERAL INFORMATION:
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LOCATION: (3787)..(5847)
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ORGANISM: Escherichia
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LENGTH: 14483
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                                                       Indels
                               Score 814.2; DB 6;
Pred. No. 1.6e-146;
0; Mismatches 758;
                               27.3%; 63.0%;
                                                        Conservative
                                            Best_Local Similarity
Matches 1312; Conser
; OTHER INFORMATION:
US-10-216-289-3
                                  Query Match
Best Local S
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ACATITCAAAAATACCGATAAICTAAGATTATGCAACACCATTTCGATTTTTAGCGG 4790
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APPLICANT: NINOMITA, TOSHIO

APPLICANT: SUGIURA, NOBUO

APPLICANT: KIMATA, KOJI

TITLE CANT: KIMATA, KOJI

TITLE COF INVENTION: CHONDROTIIN POLYMERASE AND DNA ENCODING THE SAME
FILE REFERENCE: J26882US

CURRENT APPLICATION NUMBER: US/10/216,289

CURRENT APPLICATION NUMBER: JP 2001-244685

PRIOR PILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-20

PRIOR PILING DATE: 2001-02-2

PRIOR PILING DATE: 2001-02-2

PRIOR PILING DATE: 2002-04-05

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.1 Length 2058; Indels Score 807.2; DB 6; Pred. No. 3.1e-145; 0; Mismatches 743; Sequence 1, Application US/10216289 GENERAL INFORMATION: 27.1%; 63.2%; Query Match
Best Local Similarity 63.2
Matches 1296; Conservative TYPE: DNA ORGANISM: Escherichia coli LOCATION: (1)..(20 OTHER INFORMATION: NAME/KEY: CDS 2058 LOCATION: SEQ ID NO 1 235 421 355 480 536 181 301 361

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US-09-134-000C-2987
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                                                   836 AAGACAATGATATTGTTTTAATTGGACCTAGAAAATATGTGGGATACTCATAATATTACCG
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BENTERCOCCUS FAECALIS FOR
FILLE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
GURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
NUMBER: OF SEQ ID NOS: 6812
SEQ ID NO 2987
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US-09-134-000C-2987
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APPLICANT: Gilbert, Michel
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CURRENT APPLICATION NUMBER: US/02/816,028
PRIOR PILING DATE: 2002-11-21
PRIOR PLILING DATE: 1999-01-03-21
PRIOR PLILOR GATE: 1999-02-01
PRIOR PLILOR DATE: 1999-02-01
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14.2
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APPLICANT: National Research Council of Canada
1654 CTGTGTTTAAAAGAATTTTTAAAAGA 1679
                                     319 CTATTATATACAAATATCGTAAAAGA 344
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; Sequence 1, Application US/10303161
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
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Best Local Similarity 51.2%;
Matches 211; Conservative (
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US-10-303-162-1/c
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APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wational Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFERENCE: 019633-0001110S
CURRENT APPLICATION NUMBER: US/10/303,118
PRIOR APPLICATION NUMBER: US/09/816,028
PRIOR FILING DATE: 2001-31-21
PRIOR FILING DATE: 1099-02-01
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APPLICANT: Wakarchuk, Warren W.

APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of TITLE OF INVENTION: Canapylobacter Glycosyltransferases for Biosynthesis of TITLE OF INVENTION: Canapylobacter Glycosyltransferases of Canapylobacter 105-03-0011103
CURRENT APPLICATION NUMBER: US/09/816,028
PRIOR FILING DATE: 2001-103-21
PRIOR PLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
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                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO.1
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Matches 211;
        US-10-303-128-1
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APPLICANT: Gilbert, Michel
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wational Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFREENCE: 019633-0001110S
CURRENT APPLICATION NUMBER: US/10/303,128
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/816,028
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 2000-01-31
NUMBER: US 09/495,406
PRIOR FILING DATE: 2000-01-31
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                                                                                                                                                                                OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384 OTHER INFORMATION: including LOS biosynthesis locus
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PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1
LENGTH: 11474
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                                                                                                                      TYPE: DNA
ORGANISM: Campylobacter jejuni
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FEATURE:
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SEQ ID NO 1
LENGTH: 11474
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Glibert, Michel

APPLICANT: Wakarchuk, Warren W.

APPLICANT: Watarchuk, Warren W.

APPLICANT: Mational Research Council of Canada

TITLE OF INVENTION: Campylobacter Glycosyltransferases for Blosynthesis of

TITLE OF INVENTION: Gampylobacter Glycosyltransferases for Blosynthesis of

FILE REFERENCE: 01963-001110S

CURRENT APPLICATION NUMBER: US/09/416,028

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 1999-02-01

PRIOR FILING DATE: 1999-02-01

PRIOR FILING DATE: 2000-01-31
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   Score 79.2; DB 6;
Pred. No. 1.8e-06;
                                                             0; Mismatches
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                                                                Conservative
                                Similarity
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LENGTH: 11474
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11364 GCCACAACTTTCTAICATAATCCCGCTTTTTAATTCTTGCGATTTTAICTCAAGAGCTTT
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Pred. No. 4.3e-06;
0; Mismatches 543;
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SEQUERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander:
APPLICANT: DIEBENBROCK, Christian
APPLICANT: PIEBENBROCK, Christian
APPLICANT: DIEBENBROCK, Christian
APPLICANT: DIEBENBROCK, Christian
APPLICANT: Diagnosis of Diseases Assorting the Company of the Co
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Best Local Similarity 43.9%;
Matches 434; Conservative (
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                         TTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTAATAAAAACTGAGGCACA 2411
CAATATTATTGAATATAAAAAAAATATATTCGTTATTATTATTCTACATGTTGATAAGAATCA 2291
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APPLICANT: Havukkala, Ilkka J
APPLICANT: Havukkala, Ilkka J
APPLICANT: Lubbers, Mark William
APPLICANT: Lubbers, Mark William
APPLICANT: Dekker, James
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: Lhem, and methods for using them.
FILE REFERENCE: 11000.1043c3
CURRENT APPLICATION NUMBER: US/10/264,213
CURRENT FILING DATE: 2002-10-03
NUMBER OF SEQ. ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
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Drosophil

Drosophil T3 end of

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Title: Perfect score:

Run on:

Sequence:

Scoring table:

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Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDCP is constructing a physical map of the Drosophila melanogaster genome.using these BACs. For further information please see http://www.fruifiy.org The BDCP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL069706
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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CNSO020G
AL514901
CNSO167M
A0897537
CNSO18BG
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CNSO18BG
CNSO109DO
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Description

AL212733 Tetraodon BQ876453 AGENCOURT AL419462 T3 end of BG85775 1024040G1 BF272396 GA_ED001 AZ533768 ENTDC17TR

AL106171 Drosophil AL228940 Tetraodon AL071865 Drosophil BM416130 OP21217 M

ALIO5023 Drosophil ALO6362 Drosophil ALO6340 Drosophil ALO6940 Drosophil ALO6940 Drosophil ALIO9126 Drosophil ALIO9126 Drosophil BIII02 F19C22-T7 I ALA36389 T7 end of ALA36389 T7 end of ALA36389 T7 end of ALA36349 T7 end of ALA3640 Drosophil ALO63410 Drosophil ALO63410 Drosophil ALO6350 Schmidtea ALO63440 Drosophil ALO6356 ALS66565 B10881 F2446-Sp6.1

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EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                            2023 TCATTAAATAGACAAGGCATCAATTATTATAATTATGACAAATTTGATGATTAGATGAA 2082
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        2323 GCTTTCTATCATAAGCACCAAGTGAATATTTTACTAAATAATGACATCTCATATTACACG
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9
                                                                                                                                                                        Length 1101;
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                                                                                                                                           others
                                                                                                                                                                                              Indels
                                                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:727"
/clone="BACR29B23"
/clone=11b="RPCI-98"
/note="end:T7"
                                                                                                                                           232
                                                                                                                                                                          DB 17;
                                                                                                                                                                                              310;
                                                                                                                                                                          Score 93.4; DB 17
Pred. No. 4.7e-08;
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3.1%; Score 93.4; DE
al Similarity 34.3%; Pred. No. 4.7e-
226; Conservative 117; Mismatches
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Ada_xrof="taxon:36090"

Ada_xrof="taxon:36090"

Aclone_lib="Mixed Stage EST's from Globodera pallida, the potato cyst nematode"

Anote="vector: lambda GT11; This is a collaborative effort Anote—vector: lambda GT11; This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                       1 (bases 1 to 910)

Heer, J., Sosinski, B., Pokrzywa, R.M., Warry, A. and Opperman, C. Mixed Stage Egr's from Globodera pallida, the potato cyst nematode Unpublished (2001)

Contact: Opperman, C. Contact: Opperman, C. Center for the Biology of Nematode Parasitism

NC State University; IACR-Rothamsted

Campus Box 7616; Raleigh, NC 27695, USA

Tel: 919.515.9500
                           Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 TCGGAGAACGCAGAAATCAGAAAGGTGGAACTAGTACCCAAAGATTTTCCTAAAGATCTT
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                                              Tylencholdea; Heteroderidae; Heteroderinae; Globodera
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Pred. No. 8.8e-07;
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28 c 11
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Globodera pallida.
Globodera pallida
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Listed (10-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr

- Wab : www.genoscope.cns.fr

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDCP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Pieter de Jon's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial isogenic strain v2; cn bw sp, the same strain used for the BDGP's pland by to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                        Jy6 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR31021 of RPCI-98 library from Drosophila melanogaster (fruit AL071063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2319 ATTGGCTT-TCTATCATAAGCACCAAGTGAATATTTTACTAAATAATGACATCTCATATT_23377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           539 AAAAARATMAWAAATAATAAAAAAAAAAAAAAWATWAHWAHTWMATATTTWAAAAAAAW 598
                   Drosophila melanogaster.
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                   661 AAATACGAACAAAACTTGACATAAAGTATGTAAGACAAAAAGATTATGGATATCAA 717
                                                                                                                                         2.8%; Score 82.8; DB 17; Length 996; 38.8%; Pred. No. 5.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70; Mismatches 240; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-98"
/note="end : TET3"
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/organism="Trypanosoma brucei"
/strain="Trypanosoma brucei"
/strain="Trypanosoma brucei"
/db_rafe="Laboraci:5691"
/clone="Sheared DNA-46J23"
/clone="Sheared DNA-46J23"
/clone="Sheared DNA-46J23"
/clone="Sheared DNA-46J23"
/clone="Sheared DNA-8514e_1: SMaI; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb).
The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sheared DNA-46J23.TR Sheared DNA Trypanosoma brucel genomic clone AQ946120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       El-Gayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujil, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Fraser,C. and Adams,M.
Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/. Seq primer: Mi3-Reverse Class: shotgun.
ACACGAGTAATAGACTAATAAAAACTGAGGCACATTTAAGTAATATAATAAATTAAGTC 2437
                                                                                                                            AGTTAAATCTAAATTGTGAATACATCATTTTTGATAATCATGACAGCCTATTCGTTAAAA 2497
                                                                                                                                                                                                                                                   2498 ATGACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAATTTCTCAGCATTAACAC 2557
                                                                                                                                                                                                                                                                                                                                                                               ATGATTGGATCGAGAAAATCAATGCGCATCCACCATTTAAAAAGCTGATTAAAAACCTATT 2617
                                                              Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Other_GSSS: Sheared DNA-46J23.TF
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2618 TTAATGACAATGACTTAAGAAGTATGAA 2645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KWAATWAWAAAAWATTTTTTTTATWAA 986
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GSS.
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Query Match

BASE COUNT

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Best Loca Matches

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/do.xter="taxous:3033"
/clone_lib="Plasmodium falciparum 3D7 asexual cDNA"
/lab_host="Plub100 (Gaehedo, Invitrogen, Inc.)"
/lab_host="Bull00 (Gaehedo, Invitrogen, Inc.)"
/lab_host="Bull00 (Gaehedo, Invitrogen, Inc.)"
/note="Weetor: pBluescript SK plus; Site_l: EcoRi; Site_l: EcoRi; Site_l: EcoRi; Site_l: EcoRi; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage saponin(0.1%)-lysed P. falciparum 3D7 infected acrytheoytes by the acidic quanidinium-phenol chloroform method. The poly A+ RNA was isolated by the polyAT-Tract mRNA isolation system (Promega, WI) using streptavidin Magnesphere particles. Directional cDNA libraries were constructed by oligo d(T) priming of poly(A)+ RNA (5mg) into EcoRI and XhoI sites of I ZapII vector using the Zap cDNA synthesis kit (Stragene, CA). The average size of the CDNA synthesis kit (Stragene, CA). The average size of the CDNA inserts in the library was between 1.0 and 1.5%b. Clones were mass excised using the ExAssist helper phage (Stratagene), the phagemids were precititated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH100 cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 562;
                                                                                                                                                             Email: estewatson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA
Washington University Genome Sequencing Center For
Obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -400P from Gibco
                                               Washington University School of Medicine
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                 1. 562
/organism="Plasmodium falciparum"
/db_xref="taxon:5833"
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Pred. No. 1.9e-05;
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Location/Qualiflers
Unpublished (2001)
Contact: L. David Sibley
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Fax: 314 286 1810
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Plasmodium falciparum

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Tang, K., Cole, R., Chakrabarti, D., Haywood, R., Clifton, S., Pape, D.,

Barra, M., Hillier, L., Martin, J., Wylle, T., Dante, M., Theislang, B.,

Bowers, Y., Gibbons, M., Ritter, B., Bennett, J., Jentes, E., Ronko, I.,

Tsagareishvili, R., Belaygorod, L., Franklin, C., Carr, L., Grow, A.,

Waquire, L., Richery, J., Wadkins, J., Kennedy, S., Levinso, D.,

WashUr Plasmodium EST Project
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                                                                                                                Length 641;
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                                                                                                                                   CNSO20K7 1092 bp DNA linear GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 22211 of library G from Tetraodon nigroviridis, genomic survey
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                          Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Welsenbach, J., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Welseenbach, J.
Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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169 c 165 g 262 t 113 others
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461 AAATATTGATAAAGAAAATTATTTAATAAATTTACTATATAAATTAAATCAAAACAAA 520
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; Pred. No. 3e-05;
58; Mismatches 227; Indels 0;
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/b_xref="taxon:99883"
/clone="222L11"
/clone_lib="G"
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University Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

By 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of
collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pleter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
ECORI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2: cn bw sp, the same strain used for the BDGP's
pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence T7 end of BAC:
BACKS9B23 of RPCI-98 library from Drosophila melanogaster (fruit AL069706
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2429 AATTAAGTCAGTTAAATCTAAATTGTGAATACATCATTTTTGATAATCATGACAGCCTAT 2488
                                                                                                                                      TCGTTAAAAATGACAGCTATGCTTATATGAAAAATATGATGTCGGCATGAATTTCTCAG 2548
                                                                                                                                                                                                                                                                               2549 CATTAACACATGATTGGATCGAGAAAATCAATGCGCATCCACCATTTAAAAAGCTGATTA 2608
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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/clone_lib="RPCI-98"
/note="end : T7"
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CNSO6KHQ 1169 bp DNA linear GSS 17-UNN-ZUL
T3 end of clone ATOAAO05D05 of library ATOAA from strain CBS 4311
of Saccharomyces servazzii, genomic survey sequence.
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Saccharomyces servazzii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                      GTCAATCCGGATGGTAGCTTAATCGCTAATGGTTACAATTGGCCAGAATTTTCACGAGAA
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                                                                                 77.6; DB 17;
No. 5.1e-05;
smatches 424;
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/plasmid="pBeloBAC11"
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                  /note="end : T7
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289; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                              2246 ATAATAAAATTATATTCGTTATTATTCTACATGTTGATAAGAATCATCTTACACCAGACA 2305
                                                                                                                                                                                                                                                                                                                                                                                 2306 TCAAAAAAAAATATTGGCTTTCTATCATAAGCACCAAGTGAATATTTACTAAATAATG 2365
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                                       TIGITGTAGTCAATCAGTCATTAAATAGACAAGGCATCAATTATTATAATTATGACAAAT 2065
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       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                     852 TITWIWIATATATAIWAIWHAIWIWITHIWAIWIAIWIAITATAITAIWIWITHIAIT
                                                                                                                                                                                                                                                                                                                                                  732 WITIT----AAWITATWIATWATWITWITWITTITITITITITTTWAAAITAIT
                                                                                                                                                                            2126 AAATGGATATGTTAAAAGATCTTAAACTCATTCAAAATAAAGATGCCAAAATCGCAGTCA
                                                                                                                                                                                                                                               TATTCGTTAAAAATGACAGCTATGCTTATATGAAAAAATATGATGTCGG 2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/db_xref="taxon:727"
/clone="BaCN01115"
/clone_lib="DrosBAC"
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL

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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNSO4NOJ 994 bp DNA linear GSS 21-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 12204 of library G from Tetraodon nigroviridis, genomic survey.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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(bases 1 to 994)

Roest-Crollius, H. Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                      GGCACATTTAAGTAATATTAATTAAGTCAGTTAAATCTAAATTGTGAATACATCAT 2465
                                                                                                                                                                                                                                                                              783 TATTTAT-ATAAAAAWAAAAAAAAAWATAAATTTTATAAATTATAAAAANATATATT
                                                                                                                                                              GAATATTTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTAATAAAAACTGA
                                                                    2286 GAATCATCTTACACCAGACATCAAAAAGAAATATTGGCTTTCTATCATAAGCACCAAGT
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/db_xref="taxon:99883"
/clone="122P04"
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/clone_lib="g"
/clone_lib="g"
/clone_lib="g"
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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Submitted (12-APR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (E-mail:
8 segreféqenoscope.ons.fr - Web : www.genoscope.ons.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazil, 29gosaccharomyces rouxii,
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                               Jouciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bouciet, J.L., Aigle, M., Bon, E., Brottier, P., Casaregola, S., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., Bolotin-Fukuhara, M., Durens, P., Lepilale, A., Liorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S. Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
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                                                                                                                                                                                                                                                                                                                  Casaregola,S., Lepingle,A., Bon,E., Neuveglise,C., Nguyen,H., Artiguenave,F., Wincker,P. and Gaillardin,C. Genomic exploration of the hemiascomycetous yeasts: 7. Saccharomyces servazzii
FEBS Lett. 487 (1), 47-51 (2000)
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43.5%; Pred. No. 5.5e-05;
ive 26; Mismatches 294; Indels 4;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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chauser@duke.edu.
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                     CGGATGGTAGCTTAATCGCTAATGGTTACAATTGGCCAGAATTTTCACGAGAAAAACTCA
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Ahote—"Vector: pBluescript II SK-; Site_I: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAPP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in the
light, TAP medium in the dark, HS (minimal) medium in n
ambient levels of CO2 and HS medium bubbled with 5% CO2
polyA mRNA was purified from each sample, pooled and cDNA
synthesized. The CDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5′) and XhoI (3′) sites.
pBluescript II SK- plasmids were excised from the lambda
pBluescript II SK- plasmids were excised from the lambda
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
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McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durke University
Durke University
Fax: 919 613 8159
Fax: 919 613 8177
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                                                                                                                                                                                                                                                                                                                                                                                                    /strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="C. reinhardtii CC-1690,
II"
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Pred. No. 8.7e-05;
0; Mismatches 291;
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Query Match
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Tel:als 145-503-9111, Pax:81-45-503-9170)
Was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                              Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-045107.F.
Pan troglodytes
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                                                                                                                                                           GSS 02-NOV-2001
                                                                                                                                                          778 bp DNA linear GSS 02-NOV-200 clone: PTB-045107.F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
19 c 64 g 130 t 29 others
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                                                                                                                                                                                                                                                                                                                                                     Fujiyama,A., Hattori,M., Toyoda,A., T
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-045107.F"
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R.Site 2
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BH391984 B32 bp DNA linear GSS 11-DEC-2001
AG-ND-138G17.TR ND-TAM Anopheles gambiae genomic clone AG-ND-138G17
, DNA sequence.
H391984
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Shetty,J., Malek,J., Roo,H., Collins,F., Gardner,M. and Loftus,B.J.
Shetty,J., Malek,J., Roo,H., Collins,F., Gardner,M. and Loftus,B.J.
Direct Submission of BAC-end sequences from Anopheles gambiae
Unpublished (2001)
Other_GSSs: AG-ND-138G17_TF.1
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 3543
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This clone is from an A. gambiae BAC library (ND-TAM) provided by
This clone is from an A. gambiae BAC library (ND-TAM) provided by
The Clone is from a sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                       2275 CATGITGATAAGAATCATCITACACCAGACATCAAAAAAGAAATATTGGCITICTATCAT 2334
                                                                                                                                                                              AAGCACCAAGTGAATATTTACTAAATAATGACATCTCATATTACACGAGTAATAGACTA 2394
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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46.1%; Pred. No. 0.00011;
Live 0; Mismatches 340; Indels
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    /organism="Anopheles gambiae"

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/clone_lib="ND-TAM"
/note="Vector: pECBAC1
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Seq primer: M13 Rev
Class: BAC ends.
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Matches 294; Conservative
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ALO61936
ALO61936.1 GI:4940214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  b: www.genoscope.cns.fr)
rmination of this BAC-end sequence was carried out as part of a boration with the Berkeley Drosophila Genome Project (BDGP).
BDGP is constructing a physical map of the Drosophila nogaster genome using these BACs. For further information se see http://www.fruitfly.org The BDGP Drosophila nogaster BAC ibrary was prepared by Kazutoyo Osoegawa and m Mammoser in Pieter de Jong's laboratory in the Department of er Genetics at the Roswell Park Cancer Institute in Buffalo, The library is named RPCI-98 and was constructed by partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ct Submission
itted (02-JUN-1999) Genoscope - Centre National de Sequencage
91 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                    CATGITGATAAGAATCAT ---- CITACACCAGACATCAAAAAAGAAATATTGGCTTTCTA 2330
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                                  AAGAAACICGGCATICAAAAGAAAAACCATITIGIIGIAGICAAICAGICAIIAAAIAGA 2034
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
2331 TCATAAGCACCAAGTGAATATTTTACTAAATAATGACATCTCATATTACACGAGTAATAG
                                                                                        CAAGGCATCAATTATTATAATTATGACAAATTTGATGATTTAGATGAAAGTAGAAAGTAT
                                                                                                                                             ATCTTCAATAAAACCGCTGAATATCAAGAAGAAATGGATATGTTAAAAGATCTTAAAACTC
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                                                                                                                  ATTCAAAATAAAGATGCCAAAATCGCAGTCAGTATTTTCTATCCCAATACATTAAAAGGC
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EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                             2.6%; Score 76;
40.1%; Pred. No.
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Drosophila melanogaster genome survey sequence SP6 end of BACL BACNISC23 of DrosBAC library from Drosophila melanogaster (fruit ALI), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                          Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2048 ATTATAATTATGACAAATTTGATGATTTAGATGAAAGTAGAAAGTATATCTTCAATAAAA 2107
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                                                                                                                                                                                                Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 34.5%; Score 75.8; DB 17; Length 1001; Similarity 34.5%; Pred. No. 0.00011; 55; Conservative 96; Mismatches 213; Indels 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
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a 219 c 134 g 150 t 232 otl
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Search completed: January 4, 2003, 00:35:28 Job time : 3720 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

January 4, 2003, 00:35:34 ; Search time 118 Seconds (without alignments) 1089.719 Million cell updates/sec Run on:

US-09-842-484A-2 5089 1 MNTLSQAIKAYNSNDYELAL......SAKKGENIPVNKFIINSITL 965 Perfect score:

Scoring table: Sequence:

908470 seqs, 133250620 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_101002:

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					COTATATA		
		æ					
Result		Query					
Мо.	Score	Match	re Match Length DB I	DB	ID	Description	
-	5083	100.0	-	21	AAY96213	P. multocida chond	
7	5089	100.0	•	23	AAM47335	Pasteurella multoc	
٣	5067	9.66	•	23	AAM47336	Pasteurella multoc	
4	4486.5	88.2	•	20	AAY06212	Pasteurella multoc	
S	4486.5	88.2	972	21	AAY43099	P. multocida hyalu	
9	3079	60.5	•	21	AAY96212	P. multocida hvalu	
7	292.5	5.7		23	ABB48565	Listeria monocytod	
80	276.5	5.4	•	22	AAU33454	Enterococcus faeca	
6	276.5	5.4	•	22	AAU34918	Enterococcus faeca	
10	253	5.0	.,	23	ABP26805	Streptococcus poly	

Putative glycosylt CpslI protein whic S.thermophilus exo S.thermophilus exo Enzyme EPSS involv Amino acid sequeon	Amino acid sequenc Staphylococcus epi Enzyme EPSB which Amino acid sequenc CpslK protein whic Streptococcus pneu S neumoniae SP11	⊏ರ್⊏ರ್∻	Nelsseria meningit Enzyme EPSJ involv Amino acid sequenc N. gonorrhoeae gly Nelsseria polyglyc N. gonorrhoeae gly Lipo-oligosacchari Campylobacter jeju	000
2 AAB96313 1 AAY68974 8 AAW14078 8 AAW22177 1 AAY54079 1 AAY54079	21 AAY 3773 23 ABP 3922 23 ABP 3922 21 AAY 4072 21 AAY 68976 21 AAY 68976 33 APP 44656		23 AAU/2923 21 AAY54095 21 AAY3797 17 AAR91311 18 AAW96576 18 AAW06579 21 AAY97203	1 AAY97206 1 AAY81720 2 AAB47427 1 AAY97202 2 AAB47426 1 AAY97213 3 ABB53510
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11 12 14 15 16	22 22 23 24 24	255 26 28 30 30 65	332 334 34 34 38	0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

Chondroitan synthase; CS; enzyme; hyaluronic acid; ulcer; tissue abrasion; viscoelastic replacement; bloadhesive. AAY96213 standard; Protein; 965 AA. P. multocida chondroitan synthase. 17-AUG-2000 (first entry) AAY96213; RESULT 1 AAY96213

Pasteurella multocida WO200027437-A2. 18-MAY-2000.

99WO-US26501. 98US-0107929. 99US-0283402. (OKLA) UNIV OKLAHOMA STATE. DeAngelis PL;

11-NOV-1998; 01-APR-1999; 10-NOV-1999;

WPI; 2000-376319/32. N-PSDB; AAA27449.

Novel method for the enzymatic transfer of sugar molecules to an acceptor, useful for synthesis of e.g. polysaccharide bioadhesives or

us-09-842-484a-2.rag

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901
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                                   The present sequence is the Pasteurella multocida chondroitan synthase PmCS. PmCS catalyses glycosaminoglycan polymerisation to produce chondroitan: a linear polysaccharide which has viscoelastic properties which makes it useful for a number of applications. Chondroitan can be used with hyaluronic acid (HA) to coat medical devices e.g. catheters and sensors to reduce tissue abrasion. In addition, they can be used as bloadhesives for haemostatic sealing and healing of wounds and surgical incisions; and as blomaterials that provide sustained delivery of encapsulated drugs, to wounds, ulcers, injuries or surgical sites.
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 965; Conservative 0; Mismatches
delivery systems, including hybrid
                       86pp; English.
                       Claim 15; Page 85;
                                                                                                                                                   965 AA;
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The present invention relates to the coding sequence of the Pasteurella multocida chondroitin synthase. A chondroitin polysaccharide may be used as a hyaluronan polysaccharide substitute in medial or cometic applications, for example in eye or joint applications, for moisturiser or wound dressings. The enzyme may be used in covalently coupling specific drugs, proteins or toxins to the structurally moistied chondroitin for general or targeted drug delivery or radiological chondroitin for general or targeted drug delivery or radiological procedures, covalently cross linking the hyaluronic acid itself or to other supports to achieve a gel or other three dimensional biomaterial with stronger physical properties, and covalently linking hyaluronic acid to a surface to create a biocompatible film or monolayer. The present sequence is one version of the protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chondroitin synthase; dermatan sulphate; chondroitin sulphate polymer; eye application; joint application; moisturiser; drug delivery; wound dressing; biocompatible film.
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                                                                    KTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNEN
                                                                                       GEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKEKVPYIYRK
                                          LLPIEDSHIHRIPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVI
                                                                                                      IENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQG
                           pmHAS; hyaluronic acid; hyaluronan
                                                                                                                                                                                                                                                                                                  Pasteurella multocida hyaluronate synthase
                                                                                                                                                                                                                                                                    972 AA
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                                                                                                                                                                                                                                                                   AAY06212 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                     98WO-US23153
                                                                                                                                                                                                                                                                                                                                                               98US-0178851
97US-0064435
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                             Hyaluronate synthase;
                                                                                                                                                                                                                                                                                                                       Pasteurella multocida
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This present sequence represents the hyaluronate synthase (pmHAS)

of Pasteurella multocida Carter Type A. The pmHAS enzyme has

different kinetic optima with respect to pH and metal ion

dependence, and different Km values compared with the HAS enzymes

of Streptococcus equisimilis (see AAV06206) and Streptococcus

pyogenes. Km values are about 2- to 3-fold lower for UDP sugars,

on Vmax values are about 2- to 3-fold higher. The invention

provides recombinant vectors containing hyaluronate synthase DNA,

capecially S. equisimilis hyaluronate synthase DNA,

capecially S. equisimilis hyaluronate synthase DNA,

cand prokaryotic or eukaryotic host cells which produce the enzyme

and its hyaluronic acid product, particularly, a product with

modified structure or molecular size. The hyaluronic acid produced

this way is purer than that produced by conventional methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594 TDGFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN 653
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                                                                                            Nucleic acid encoding hyaluronate synthase for production of hyaluronic acid with controlled molecular weight and targeting specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.2%; Score 4486.5;
86.6%; Pred. No. 0;
:ive 63; Mismatches
                                                                                                                                                                                                     Disclosure; Page 123-125; 125pp; English.
Weigel PH;
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42; Conservative
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  Kumari
                                             WPI; 1999-337486/28.
N-PSDB; AAX58857.
    DeAngelis P,
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Matches 842;
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This is the Pasturella multocida hyaluronate synthase (PmHAS) amino acid sequence. Hyaluronic acid (HA) or hyaluronan, is a polysaccharide that serves both structural and recognition roles in higher animals. Bacteria produce extracellular capsules of HA which mimic their host HA and aid escape from a host immune response. The invention includes a vector containing the PmHAS nucleotide sequence which can be used to express PmHAS in a foreign host. The HS nucleic acids can be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccines
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                                               NTLNGLVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYY 773
TSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGMNFSALTH
                                                                                                                                                                                DWIEKINAHPPFKKLIKTYFNDNDLRSMNVKGASQGMFMKYALPHELLTIIKEVITSCQS
                                                                                                                                                                                                                               IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSTLTYMPWERKLQWTNEQIQSAKKGENI
                                   QSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYP
                                                                                                                                                                                                                                                                                                                                                                                                                                       multocida hyaluronate synthase (PmHAS) amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hyaluronate synthase; PmHAS; hyaluronan; hyaluronic acid; HA; drug delivery; anglogenesis; wound healing; capsule synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated hyaluronate synthase nucleic acids, used for the production of hyaluronic acid, for developing antibiotics and
                                                                                                                                                                                                                                                                                                                                                                 AAY43099 standard; Protein; 972 AA.
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N-PSDB; AAZ35589.
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production of HA. Also, specific changes to the HS coding sequence can result in the production of HA having a modified size distribution or structural configuration and functional properties. The HA products can be used in e.g. drug delivery, angiogenesis and wound healing, stabilisation of recombinant proteins and in cosmetics. The HS nucleic pacids can also be used to develop agents to block capsule synthesis by pathogens and act as antibiotics. The avirulent P. multocida strains can be used as vaccines for fowl cholera or shipping fever.
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                                                                                                                               Length
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                                                                                                                                DB 21;
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                                                                                                                              Score 4486.5;
Pred. No. 0;
63; Mismatches
                                                                                                                              88.2%;
86.6%;
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Matches 842; Conservative
                                                                                                         972 AA;
                                                                                                         Sequence
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ETATININPSITSKGNISLDWRLEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNKVGWFD 353
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                                                                                                                                                                 Antibacterial; gene therapy; vaccine; blosynthesis; blodegradation; vitamin B12; bacterial infection; disease.
                        1 MNTLSQAIKAYNSNDYELALKLFEKSAETYGRKIVEFQIIKCKEKL----STNS---YVS 53
                                         LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHL
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58; Mismatches
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   579; Conservative
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ABB48565
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                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the soluble recombinant form of Pasteurella multocida hyaluronic acid synthase-D, PuRAS-D. This sequence encompasses residues 1 to 703 of the 972 residues of the native PuRAS-D. This sequence encompasses catalyses glycosaminoglycan polymerisation to produce hyaluronic acid, catalyses glycosaminoglycan polymerisation to produce hyaluronic acid, at useful for a number of applications. HA can be used during ophthalmic surgery as a viscoelastic replacement for the vitreous humour e.g. during laplantation of intraocular lenses in cataract patients. HA injections directly into joints is also used to alleviate pain associated with a cathritis. HA can also be used to coat medical devices e.g. catheters and sensors to reduce tissue abrasion. HA can also be used as bloadhesives for haemostatic sealing and healing of wounds and surgical indislons; and surginal indislons; and wounds, ulcers, injuries or surgined delivery of encapsulated cuns, therefore be used to produce HA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel method for the enzymatic transfer of sugar molecules to an acceptor, useful for synthesis of e.g. polysaccharide bioadhesives or drug delivery systems, including hybrid molecules
         DWIEKTNAHPPFKKLIKTYFNDNDLKSMNVKGASQGMFMTYALAHELLTIIKEVITSCQS
                                                      901 IDSVPEYNTEDIWFQPALLILEKKTGHVFNKTSTLTYMPWERKLÖWTNEQIESAKRGENI
                                       894 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSTLTYMPWERKLQWTNEQIQSAKKGENI
                                                                                                                                                                                                                                                                                                                                        HAS-D; enzyme; ophthalmic surgery; tissue abrasion; bioadhesive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 702;
                                                                                                                                                                                                                                                                                                                                        Hyaluronic acid synthase-D; HAS-D; enzyme; ophthalmik
cataract; arthritis; ulcer; tissue abrasion; bloadhek
viscoelastic replacement; hyaluronic acid production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 3079; DB 21;
Pred. No. 1.2e-227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "encoded by AACTGT"
                                                                                                                                                                                                                                                                                                            multocida hyaluronic acid synthase-D.
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
Misc-difference 450
                                                                                                                                                                                                                 AAY96212 standard; Protein; 702 AA.
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82.4%;
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99US-0283402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US26501
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         Pasteurella multocida
                                                                                                         PVNKFIINSITL 965
                                                                                                                             PVNKFIINSITL 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-376319/32.
N-PSDB; AAA27448.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DeAngelis PL;
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01-APR-1999;
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                  841
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593

533

473

(first entry)

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Enterococcus faecalis cellular proliferation protein #90.
                                                                                                                            Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                   21-MAR-2001; 2001WO-US09180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                       Enterococcus faecalis.
                                                                                                                                                                                                                          WO200170955-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-2000;
22-DEC-2000;
                                                     14-FEB-2002
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                 AAU33454;
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                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the genome sequence of Listeria monocytogenes ECD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                     Dehoux P;
Cossart P;
                                                                                                                                                                                                                                                              Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides
                                                                                                        , Amend A;
Durant L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FEKENGGQATARNFGLDVATGDYIVMVDSDDYISKNLVETCL-DTVQKTNADLVLFTSYN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                493 MSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNRN 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------LIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGF--- 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -NENIENAVDY - - - DMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKN 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            648 HFVVVNÅDSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDL---KLIQNKDA 704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 PLVSVIIPVYNVEKYVRCLDSVLEQTYHNLEVIVVNDGATDNSAKVIKSISDN--RIRY 60
                                                                                                                                                                   Hauf J;
                                               C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; ernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A T, Domann E, Haln T, Berche P, Charbit A, Durant L; J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           705 KIAVSIFYPNTLNGLVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKH 760
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                                                                                                                                                                                                                                                                                                                                        Claim 6; SEQ ID No 1270; 192pp; French.
                                                                    Dussury.

Daniels J, Goeuc.

Dominguez-Bernal G, Garriuu.
Chakraborty T, Domann E, H.
Perez-Diaz J, Baquero F, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98; Conservative
               (INSP ) INST PASTEUR.
                                                                                                                                                                                                                        WPI; 2002-010914/01.
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                                                     Buchrieser C,
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Carr GJ;

Wall D, Trawick JD,

Zyskind JW,

Ohlsen KL,

2000US-207727P. 2000US-242578P. 2000US-253625P. 2000US-257931P. 2001US-269308P.

2000US-191078P. 2000US-206848P.

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are genes themselves and the encoded proteins. The prokaryotes used are cascherichia coli, Staphylococcus aucus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The commention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen corrections on the used to screen compounds in rational drug discovery programmes uncleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

On the printed specification, but was obtained in electronic format directly from WIPO at the printed probablished_pct_sequences.
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                                                                                                                                                                                                         of
                                                                                                                                                                                                         polynucleotides for the identification and development
                                                                                                                                                                                                                                                     antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                    Example 3; Seg ID No 4950; 511pp; English.
Xu HH;
                                                                               WPI; 2001-611495/70.
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                                                                                                                      N-PSDB; AAS51313
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AAU33454 standard; Protein; 706 AA

AAU33454 ID AAU RESULT 8

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Yamamoto RT,
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                                                                                                            280 FYEVVKVLNENPELDLIXSDEDKIDMDGNRSDPAFK-PDWSPDLLLGTNXISHLGVYRRS 338
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                                                                                                                                             KLIQNKDAKIAVSIFYPNTLNG---LVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEI
                                                                                                                                                                                                                                   754 LAFYHKHQVNILLNN-DISYYTSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFVK
                                                                                                                                                                                                                                              488 AKFEQQLPGREFVESIDIPF------NESTINNRAAKKAHGEYLLELNNDTEVIT
                                                                                                   330 VELCLKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIR
                                                                                                                                  590 AWHLTDGFNENIENAVDYDMFLKLSE---VGKFKHLNKICYNRVLHGDNTSIKK--LGIQ
                                                                                                                                                                   645 KKNHFVVVNQSLNRQGINYYN----YDKFDDLDESRKYIFNKTAEYQEEMDMLKDL
                                                                                                                                                                              DEEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKE
                 -----IKAKKGFKYMAKNGIS-HTIQRAKIEKLRNQA--SYLNWLARN
                                 KVPYIYRKLLPIEDSHIHRIPLVSIYIPAYNC-ANYIQRCVDSALNQTVVDLEVCICNDG
                                            472 STD-NTLEVINKLYGNNPRVRIM-SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDA
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                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecalis cellular proliferation protein #205.
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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26-MAY-2000;
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                      DKVTRLW-
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The invention relates to antisense inhibitors of genes essential to prokaryotic callular proliferation, their use in identifying the genes, their use in the discovery of novel antiborics, the essential comes, their use in the discovery of novel antiborics, the essential comes, their use in the discovery of novel antiborics, the essential comes are themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aud Enterococcus facellis. The neumoniae, Pseudomonas acrudinosa and Enterococcus facellis. The contention is also useful for the identification of potential new targets for antibotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery corporammes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic callular proliferation protein.

Control of the printed specification, but was obtained in electronic control of the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLIQNKDAKIAVSIFYPNTLNG---LVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEI 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKVTRLW------IKAKKGFKYMAKNGIS-HTIORAKIEKLRNOA--SYLNWLARN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 DNDIVLIGPRKYVD--THNITAEQFLNDPYLIESLPETAINNNPSITSKGNISLDWR--- 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                590 AWHLTDGFNENIENAVDYDMFLKLSE---VGKFKHLNKICYNRVLHGDNTSIKK--LGIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKNHFVVVNQSLNRQGINYYN-----YDKFDDLDESRKYIFNKTAEYQEEMDMLKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKE
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                                                                                                                                         oţ
                                                                                                                                  New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                       English.
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                                                                                                                                                                                                                                       Example 3; Seq ID No 10511; 511pp;
Xu HH;
                                                       2001-611495/70
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Length 321;

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                                                                                                                                                                                                                                                                                                                                            Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
539 ENWLTLMVSFAQQERIGCVGAKLLYPNNTVQHAGVILGLGGVAGHGHYGYPHGDLGYFGR 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Masignani V, Margarit Ros YI, Grandi G,
                                                                                                       822 YDVGMNFSALTHDWI----EKINAHPPFKKLIKTYFNDNDL 858
                                                                                                                           Streptococcus polypeptide SEQ ID NO 2786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 3429; 4525pp; English.
                                                                                                                                                                                                                    ABP26805 standard; Protein; 321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                                                                                                                                                                                   (first entry)
             490 AKFEQQLPGRFFVESIDIPF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus agalactiae
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                                            ND----SYA-----
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N-PSDB; ABN67436.
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Tettelin H;
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                                                                                                                                                                  64 KNNGGLSDARNYGISRATGDYIYLLDSDDYLYKEDAIERMYEFSEKYNSEIVLGC-YVEK 122
                                                                                                                                                                                                                 R----NVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIENAV 605
                                                                                                                                                                                                                                                     204 YNTY-----AYRIRENSIMTGSYN----IKRLHAVEALKERIYLLEKYPDLVFOSER 251
                                                                                                                                             495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYL-EPDAVELCL---KEFLKDKTLACVYTTN 550
                                                                                                                                                                                                                                                                                                                                                                666 YDKFDDLDESRKYIFNK----TAEYQEEMDMLKDLKLIQNKDAKIAVSIFYPNTL----N 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 ALIKTMEVNLIELYKNNFYKEFHT----LKTEYKKTIFDFIKKQRMLLKIKYYLKYCVVH 307
                                                                       435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                     Gaps
                                                                                                                                                                                                                                                                                                                 606 DYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINYYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative glycosyltransferase, involved in cell wall biogenesis #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      718 GLVKKLN-NIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYYTSN
                                   74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry -
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                                     Indels
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Weissenbach J, Saurin W, Heilig R;
5.0%; Score 253; DB 23;
25.1%; Pred. No. 5.8e-11;
iive 64; Mismatches 142;
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(IFRE-) IFREMER INST FR RECH EXPL MER.
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                                     Conservative
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                    Similarity
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                                   94;
 Query Match
Best Local S
Matches 94
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Capsular gene cluster; serotype 1; polysaccharide biosynthesis; capsular component; antigen; regulation; chain length determination; complement mediated opsonophagocytosis; serotype-specific detection; antigen; vaccine; Streptococcal disease; CpsIE; CpsIE; CpsII; CpsI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      492 IMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLK-DKTLACVYTTN 550
                                                                                                                                                                                                                                                                                                                                                                                  433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVR- 491
                                                                                                                                                                                                                                                                                                                                                                                                                        uses, since the proteins are stable at very high temperatures, some ullO degrees centigrade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 IRLKKNSGSPIARNIGIKKAKGRFIALLDDDDEWLPHRLEVQVRKFENLGKEFGVVYGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNVNPDGSLIANGYNWPEFSREKLTTAMIAHHF-----RMFTIRAWHLTDGFNENIENAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINYYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               666 YDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYPNTLNGLVKKLN-
                                                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                             Length 298;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cps11 protein which has glycosyltransferase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:||:|::: || ::::|
DWDMMLRIARYYKFDYVDEIIAKYYVHGKQISF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
                                                                                                                                                                                                                                                             Query Match
4.9%; Score 251; DB 22;
Best Local Similarity 24.3%; Pred. No. 7.3e-11;
Matches 81; Conservative 66; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --NIIEYNKNIFVIILHVDKNHLTPDIKKEILA 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 SIAIAPLNLENYMILLKLALDSRTVEYIKRILS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY68974 standard; Protein; 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-NL00460
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                                                                                                                                                                                                            298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ60930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200005378-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUL-1998;
22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY68974;
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           551
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15;
                                                                Streptococcus suis serotype 1. The genes in this cluster are involved in polysaccharide biosynthesis of capsular components and antigens. The proteins have glycosyltransferase activities (CpsIE, CpsIG, CpsII, CpsII, and CP polymerase activities (CpsII). The capsule confers deacterium resistance to complement-mediated opsonophagocytosis. The gene cluster is used as a source of probes and primers for scrotype-specific detection of S. suis and is also useful for recombinant production of the proteins. The proteins are then useful for producing antigens that can be used in vaccines, for controlling or eradicating a Streptococcal disease, in humans or animals, e.g. against S. suis in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSIFYPNTLNGLVKKLNNIIEXN--KNIFVIILHVDKNHLT--PDIK-KEILAFYHKHQV 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -FVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIA 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 LVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIM 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          554 NPDGSLIA-----NGY-----NWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGF 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The proteins AAY68970-76 are encoded by the capsular gene cluster of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        operon; lactic acid bacterium; epsF; epsG; epsH; epsI; epsJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 GSNIEN----NVWCKLYSRDIIKDIKFQINNRSIGEDLLFNLEVLNNVTRVVVDTREYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 NYVIRNSSLINQKFSINNIDLVTRLE---NYPFKLKREFSHYF----DAKVIKEK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNRNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGD------NTSIKKLGIQKKNH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.8%; Score 246; DB 21; Length 322;
25.3%; Pred. No. 2e-10;
Live 58; Mismatches 120; Indels 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.thermophilus exopolysaccharide biosynthesis enzyme EpsH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus thermophilus strain Sfi6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exopolysaccharide biosynthesis; epsepsR; epsA; epsB; epsC; epsD; epsE; epsK; epsL; epsL; CNCM I-1590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW14078 standard; Protein; 324 AA.
Disclosure; Fig 4; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95EP-0201669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 25.3% les 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     763 NILL 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLYL 304
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AAY54079 standard; Protein; 339 AA.
                                                                                                                                                                                                                                                                            Claim 7; Page 14-28; 46pp; French
                                                                                                                                                                                                                                          DNA of lactic acid bacteria – er
exo-polysaccharide biosynthesis
                                                                                                                                     95EP-0201669.
                                             Streptococcus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      777 RLIKTE--AHLSNINK 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                             (NEST ) SOC PROD NESTLE
                                                                                                                                                                                   Mollet B, Stingele F;
                                                                                                                                                                                                         WPI; 1997-044837/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      324 AA;
                                                                                                                                                                                                                     N-PSDB; AAT73236.
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                                                                                                                                     20-JUN-1995;
                                                                  EP750043-A1
                                                                                         27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                   90;
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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AAY54079
ID AAY54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    464
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                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : |:| :: | :: | DAYDYAVQRPNSIMNSSFN------LKKLDIIE--------WYHEMENDIIA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                    661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLNNIIEYNKN-IFV----IILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYYTSN 776
                                                                                                                                                                                                                                                                                                                                                                                          LVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIM 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENI 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYPNTLNGLVK 721
                                                                                                                                                                                                                                                                                                                                                                                                        A chromosomal DNA sequence representing practically the whole eps (exopolysaccharide biosynthesis) operon from Streptococcus thermophilus strain Sf16 (deposited as CNCM r-1590) was isolated. The sequence contained 14 open reading frames, one of which was located on the complementary strand. The present sequence is decoded from the epsH open reading frame. The EpsH protein is probably a glycosyl transferase.

Novel exopolysaccharides can be produced by transforming lactic acid bacteria which produce exopolysaccharides with DNA encoding at least one enzyme from the eps operon. The new exopolysaccharides are useful for thickehing drinks, liquid desserts, yoghurts, soups, ice-creams, coffee creams, sauces, mayonnaise, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S.thermophilus exopolysaccharide synthesis operon epsI gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGI
                                                                                                                                                                                                                                                                                                                                               DB 18; Length 324;

    encoding enzymes involved

                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -------KGSLLTK----KEAPKKKSEVVSIEESIKILLLO-
                                                                                                                                                                                                                                                                                                                                             4.7%; Score 238.5; DB 18;
23.9%; Pred. No. 7.6e-10;
Live 58; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW22177 standard; Protein; 324 AA.
                                                                                                                                               Claim 7; Pages 33-34; 42pp; French
                                                                                                                         exo-polysaccharide biosynthesis
                                                                                                             ONA from lactic acid bacteria
           95EP-0201669
                                  SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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ARLKNRLGASLSFLGK 311
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                 (NEST ) SOC PROD NESTLE
                                                     Stingele F;
                                                                            WPI; 1997-044836/05.
                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                       324 AA;
                                                                                         N-PSDB; AAT62328
          20-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                    90;
                                                      Mollet B,
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Streptococcus thermophilus exopolysaccharide (EPS) synthesis operon. The operon has 13 oper reading frames (ORF) designated eps^A M encoding proteins AAW22169-81. This protein has 24% identity to a protein encoded by the RfbV ORF of the rfb cluster from Salmonella typhimurium and is probably a glycosyl transferase. The EPS are useful for thickening e.g. drinks, liquid desserts, yoghurts, soups, ice-creams, coffee creams, sauces, mayonnaise.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         represents the protein encoded by the epsI gene from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 OFPNLALYVKNRAFAAEVKIFLEIPKEKEFEQAQKOL----WH-----DIKKNRKAPFMTKG 295
Streptococcus thermophilus; operon; exopolysaccharide; synthesis; open reading frame; thickening; drink; liquid dessert; yoghurt; soup; sauce; ice-cream; coffee cream; mayonnaise; glycosyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 LVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIM 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENI 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              662 NYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYPNTLNGLVK 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 DAYDYAYVQRPNSIMNSSFN------LKKLDIIE------MVHEMENDILA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KGSLLTK----KEAPKKKSEVVSIEESIKILLLQ-
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13;

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Enzyme EPS5 involved in exopolysaccharide biosynthesis.
       (first entry)
                                                                                   WPI; 2000-097267/08
                                             W09962316-A2
                                                        22-APR-1999;
                                                             22-APR-1998;
                                                                22-APR-1998;
22-APR-1998;
                                                                             Stingele F,
       27-MAR-2000
                                                  19-DEC-1999
                                                                                                                                                                       Sequence
  AAY54079;
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AAY54075-85 represent enzymes involved in the biosynthesis of
exopolysaccharides (EPS). These enzymes are designated EPS1-EPS11 and
care encoded by open reading frames eps1-eps11. The enzymes are isolated
from Lactobacillus helveticus strain LH59. The proteins are used
from Lactobacillus helveticus strain LH59. The proteins are used
in a method for the synthesis of EPS, which includes at least one step
of forming a bond (alpha or beta isomer) between C-1 (carryning the
cof forming a bond (alpha or beta isomer) between C-1 (carryning the
cof EPS cocurs with, in each step, addition of a new sugar unit, through
cof EPS occurs with, in each step, addition of a new sugar unit, through
cof IEPS occurs with, in each step, addition of a new sugar unit, through
cof its hemi-acetyl function, to an alcoholic hydroxyl of a second sugar
cof int, present at the end of a chain of sugar residues bonded to the
primer. EPS1 has homology with an undecaprenyl-phosphate-girosyl-1-
phosphate-transferase; EPS2, EPS3 and EPS4 are alpha-
cylvcosyltransferase; EPS5 and EPS6 have homology with a beta-
glycosyltransferase; EPS9 and EPS6 have homology with a beta-
cylvcosyltransferase; EPS9 and EPS6 have homology with a beta-
glycosyltransferase; EPS9 and EPS6 have popolymerase;
conto the following repetitive unit; EPS10 transports the polysaccharides
conto the following repetitive unit; EPS10 transports the polysaccharides
conto the EPS enzyme are used to improve properties of formed
particularly fermented milk products such as yoghurt and cheese,
ceg. their organoleptic properties and flavour stability.
Exopolysaccharide; EPS; ESP enzyme; EPS1; EPS2; EPS3; EPS4; EPS5; EPS1 eps7; EPS8; EPS9; EPS1; EPS1; Lactobacillus helveticus strain LH59; activated D-galactose pyranose; saccharide; beta-qlycosyltransferase; undecaprentl-phosphate-qlycosyl-1-phosphate-transferase; alpha-qlycosyltransferase; psp polymerase; qlycosyltransferase; psp polymerase; qlycosyltransferase; chesphofuranose; transporter; food; fermented milk product; yoghurt; cheese; flavour stability; organoleptic property.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properties of fermented milk products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ45259, AAY54082, AAY54083, AAY54084; AAX54085.
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98EP-0201311.
98EP-0201312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactobacillus helveticus
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17;

DB 21; Length 339; Indels

4.5%; Score 230.5; DB 21; 25.2%; Pred. No. 3.4e-09; tive 64; Mismatches 131;

Conservative

Local Similarity hes 93; Conserv

Best Loca Matches 433

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Query Match

PLVSIYIPAYNCANYIQRCVDSALNQTVVD-LEVCICNDGSTDNTLEVINKLYGNNPRVR 491

492 IMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLE------PDA--VELCLKEFL 538

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699 IQN-KDAKIAVSIFYPNTLNGLVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILA-- 755
                                                                                                                                                                                                                                                                                   279 INNDKNKKLOKEVYWQ-----AYKLKRYVFKSKSI------PVSKKMFFACT 319
                                                                             123 KLNTNNKLLEEYKFSNVTRSAEDVISLLLNETGPQGYLWNKMFR----TSIIKKYSLLLD 178
K----DKTLACVYTTN--RNVNPDGSLIAN-----GYNWPEFSREKLTTAMIAHHFRMFT
                                                                                                                                                 179 PKIF-----MAEDLLFCIQYLKFSKKVRVSNYCDYNYVQDSNSMNGGLSFTKNNRRYKKI
                                                                                                                  588 IRAWHLTDGFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHG-----DNTSIKKL
                                                                                                                                                                                   642 GIQKKNHFVVVNQSLNRQGINYYNYDKFDDLDESRKY---IFNKTAEYQEEMDMLKDLKL
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EPS3; EPS4; EPS5; EPS6;

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January 4, 2003, 02:22:39 ; Search time 66 Seconds (without alignments) 430.199 Million cell updates/sec
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5089
1 MNTLSQAIKAYNSNDYELAL......SAKKGENIPVNKFIINSITL 965
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

262574

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 3, Appli	1		10,	Sequence			Π	m	Sequence 11, Appl	m	Sequence 11, Appl	m	1	'n	æ	Sequence 3, Appli	1,	'n	Sequence 8, Appli	2	Sequence 12, Appl	Sequence 5, Appli	12,	2,	12,	2, 7
SUMMARIES	ID	US-09-437-277-3	US-09-437-277-1	US-08-597-236-10	US-08-746-682A-10	US-09-134-001C-4067	US-08-961-083-200	US-08-312-387B-3	US-08-312-387B-11	US-08-683-426-3	US-08-683-426-11	US-08-683-458-3	US-08-683-458-11	US-08-878-360-3	US-08-878-360-11	US-08-478-140B-3	US-08-478-140B-8	US-09-333-412-3	US-09-333-412-11	US-09-338-943-3	US-09-338-943-8	US-08-312-387B-5	US-08-312-387B-12	US-08-683-426-5	US-08-683-426-12	US-08-683-458-5	US-08-683-458-12	US-08-878-360-5
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dР	Query Match	100.0	60.5	4.7	4.7	4.5	4.4	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1
	Score	5089	3079	238.5	238.5	227	223.5	210	210	210	210	210	210	210	210	210	210	210	210	210	210	209	209	209	209	209	209	209
	Result No.	1	7	m	4	S	9	7	σ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

Sequence 12, Appl Sequence 5, Appl1	5,	-	Ŋ	×	Sequence 20, Appl	Sequence 15, Appl	Sequence 6, Appl1	Sequence 6, Appl1	Sequence 6, Appli	Seguence 6, Appl1	Sequence 196, App	Sequence 198, App	Sequence 2, Appli	Sequence 3159, Ap	Sequence 4051, Ap	Sequence 4452, Ap
US-08-878-360-12 US-08-478-1408-5	US-09-333-412-5	US-09-333-412-12	US-09-338-943-5	US-08-392-625-20	US-08-466-961A-20	US-08-645-193B-15	US-08-480-604A-6	US-08-405-496A-6	US-08-915-136-6	US-08-957-310-6	US-08-961-083-196	US-08-961-083-198	US-08-648-298-2	US-09-134-001C-3159	US-09-134-001C-4051	US-09-134-001C-4452
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337	337	337	337	066	066	066	2710	2710	2710	2710	281	270	633	10182	418	926
4.4	4.1	4.1	4.1	3.5	3.5	3.5	3.4	3.4	3.4	3.4	3.4	ж Э.Э	3.1	3.1	3.1	3.0
209	209	209	209	178.5	178.5	176.5	174.5	174.5	174.5	174.5	173.5	167.5	156.5	156.5	156	153.5
28 29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 (So 09-437-277-3 (Sequence 3, Application US/09437277 (Patent No. 6444447 (SERERAL INFORMATION: (APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA) (TITLE OF INVERTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHAM) (CURRENT APPLICATION NUMBER: US/09/437,277	CONCENT FIGURE OF SEC 15 OF 1 TO 1
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SES

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	bs	09	09	120	120	180	180	240	240	300	300	360	360	420	420
	Gaps														
5;	ö	DKKN	DKK	DFPK	DFPK	NON	NOK1	FVS	FVS	TAT	TAT	EFNH	EFNE	PYIY	PYIY
Length 965;	_	VSE	VSE	VPK	VPK.	CLV	CLV	KYD	KYD	LPE	LPE	FDE	FDE	EKV	EKV
ngth	Indels	INSY	INSY	KVEL	KVEL	ITLA	ITLA	LRTA	LRTA	LIES	LIES	KVGF	KVG.	KIVK	CIVE I
Lei	In	KLS	KLS	EIR	EIR	ILD	-11	NEG	SICG -	IDPY	IDPY	WLN	NE L	ITL	111
DB 4;	; 0	KCKE	KCKE	SENA	SENA	NRSB	NRSF	CAVE	CAVE	OFLA	OFL	FSKE	FSKE	AGKS	AGKS
DB	_	, oii	ij	GKK	GKK	PTF	PTF	YOU	.xor	TAE	TAE	NVA	- NA	ERE	ERE
89;	Mismatches	IVE	IVE	KSI	KSI	Siii	SIII	KDYC	KDYC	THN	THN	FVAC	FVAC	ENE	ENE
50	smat	GRK	GRK	KNKW	CNKW	AIGL	IGE -	rvro	- X	CXVD	CY.	PFRY	PERY	PPGK	PPGK
Score 5089;	Mis	AET	AET	INSE	NSE	VNK	- V	DIK	DIK	GPRI	GPR	CDS	CDS	HOE	HOE
	, ;	FEKS	FEKS	ESEK	ESEK	SIKP	SIKP	EOKL	EOKL	IVLI	IALI	NLRI	NLR	GMAI	SMAI
100.08;	ive	LKE	LKL	TLS	TLS	KSL	KSE	OKY	ŌKY∐	DNO	QNQ	KTD	KTD	IDG	-Ď
100	Conservative	YELA	YELA	VKKI	VKKI	KNRK	KNRK	LIIV	111	ELLE	ELLE	EHFK	EHEK	FFRV	FFRV
;	rva	GNS	SND	LSN	TRI	TWT.	TWY.	ENI	ENE	YLT	XILT.	WRL	WRL	KGC	KGC
1	onse	KAYN	KAY	TOLI	10E	VNDE	VND	DGSF	DGSF	WVHS	MVH5	ISE	ISE	RLF	RLF
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ch	Matches 965; Conser	MYTLSQAIKAYNSNDYELALKLFEKSAETYGRKIVEFQIIKCKEKLSTNSYVSEDKKNSV	MNTLSQAIKAYNSNDYELALKLFEKSAETYGRKIVEFQIIKCKEKLSTNSYVSEDKKNSV	CDSSLDIATQLLLSNVKKLTLSESEKNSLKNKWKSITGKKSENAEIRKVELVPKDFPKDL	CDSSLDIATQLLLSNVKKLTLSSSEKNSLKNKWKSITGKKSENAEIRKVELVPKDFPKDL	VLAPLPDHVNDFTWYKNRKKSLGIKPVNKNIGLSIIIPTFNRSRILDITLACLVNQKTNY	VLAPLPDHVNDFTWYKNRKKSLGIKPVNKNIGLSIIIPTFNRSRILDITLACLVNQKTNY	PFEVVVADDGSKENLLTIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKYDFVSILD	PFEVVVADDGSKENLLTIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKYDEVSILD	CDMAPQQLWVHSYLTELLEDNDIVLIGPRKYVDTHNITAEQFLNDPYLLESLPETATNNN	CDMAPQQLWVHSYLTELLEDNDIVLIGPRKYVDTHNITAEQFLNDPYLIESLPETATNNN	PSITSKGNISLDWRLEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNKVGWFDEEFNHWG	PSITSKGNISLDWRLEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNKVGWFDEEFNHWG	GEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKEKVPYIYRK	GEDVEFGYRLFARGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKEKVPYIYRK
Mat	S &	Ψ-	- Σ -⊣	61 C	61 C										
Query Match	tche			9	ø	121	121	181	181	241	241	301	301	361	361
Öğ	Ma	οy	qq	οy	QQ	οy	QQ	οy	Ob	οy	Dp	δy	QQ	٥y	СP
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APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fanucci A., Allan
REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRY: U.S.A.
10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-08-597-236-10
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                                                    NKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKD
                                                                 541 KTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNEN
                                                                                                             US-09-437-277-1

Sequence 1, Application US/09437277

Sequence 1, Application US/09437277

Sequence 1, Application US/09437277

GENERAL INFORMATION:
APPLICANT: THE BOARD OF RECENTS OF THE UNIVERSITY OF OKLAHOMA
TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
FILE REFERENCE: 5820.551

CURRENT APPLICATION NUMBER: US/09/437,277

CURRENT FILING DATE: 1999-11-10

NUMBER OF SEQ ID NOS: 6

SOFTWARE: WordPerfect 8.0 (saved in ASCTIT format)
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82.4%; Pred. No. 1.1e-260;
ive 58; Mismatches 58;
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US-09-437-277-1
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LENGTH: 702
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                                                                                                                      ETATINNPSITSKGNISLDWRLEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNKVGWFD
                                                                                                                                      DNTLEVINKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELC
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                                                         VNOKTNYPEEVVVADDGSKENLLTIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKY
              QSLNRQGINYXNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDL 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08597236
Fatent No. 5733765
GENERAL INFORMATION:
APPLICANT: STINGELE, Franscesca
APPLICANT: WOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODU
TITLE OF INVENTION: LACTIC BACTERIA PRODU
TITLE OF INVENTION: LACTIC BACTERIA PRODU
CORRESPONDENCE SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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STREET: 1155 Avenue of the Americans
CITY: New York
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INFORMATION FOR SEQ ID NO: 10:
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Best Local Similarity
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US-09-134-001C-4067
                                                                     LENGTH:
                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                89;
                                                                                                                                                                                                               Length 324;
                                                                                                                                                                                                       4.7%; Score 238.5; DB 1; Length : 23.9%; Pred. No. 1.2e-12;
tive 58; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| | :: | | | :: | | 156 QNGYDLAVWGKLYPVSFFETIS-FPEGKLYEDMGTTYKLLKLASEVVF---
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SOFTWARE PATENTIAN STATEM.
SOFTWARE PATENTIAN DATA:
APPLICATION NUMBER: US/08/746,682A
FILING DATE: 14-NOV-1996
CLASSIFICATION 435
PRIOR APPLICATION NUMBER: 08/597,236
FILING DATE: 20-JUN-1995
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: STINGELE, Franscesca
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXOPOLYSACCHARIDES
CORRESPONDENCE: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americans
CITY: New York
STATE: New York
COUNTRY: U.S.A.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 10, Application US/08746682A
; Patent No. 5786184
; GENERAL INFORMATION:
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REGISTRATION NUMBER: 30256
324 amino acids
amino acid
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Best Local Similarity 23.98
Matches 90; Conservative
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296 ARLKNRLGASLSFLGK 311
                                    ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-597-236-10
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THILE OF INVENTION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4067
                                                                                                                                                                                                                                                                         13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 QFPNLALYVKNRAFAAEVKIFLEIPKEKEFEQAQKQL----WH----DIKKNRKAPFMTKG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------KGSLLTK----KEAPKKKSEVVSIEESIKILLLQ------- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 QNGYDLAVWGKLYPVSFFETIS-FPEGKLYEDMGTTYKLLKLASEVVF-----L 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  722 KLNNIIEYNKN-IFV----IILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYYTSN 776
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                                                                                                                                                                                                                                                                                                                                    434 LVSIYIPPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIM 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                         494 SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVE------LCLKEFLKDK 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    542 TLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENI 601
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22.8%; Pred. No. 4.4e-11;
tive 66; Mismatches 161; Indels 192;
                                                                                                                                                                                                                Length 324;
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                                                                                                                                                                                                             4.7%; Score 238.5; DB 1; 23.9%; Pred. No. 1.2e-12; tive 58; Mismatches 139;
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                               : 324 amino acids
amino acid
                                                                                                                                                                                                                                         Best Local Similarity 23.9%
Matches 90; Conservative
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SEQUENCE CHARACTERISTICS
                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-746-682A-10
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823 -----DVGMNFSALTHDWIEKINAHPPF---KKLIKTYFND------NDLRSMNVK 864
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                                                                                                                                                                                                                            204 FNFPFFFRGEVYDPFETLTLS-------EQNFDILFKDY------VNSFYD 241
                                                                                                                                                                                                                                                                -PNTLNGLVKKLNNII-----EYNKNIFVIILHVDKNHLTPDIKKEILAFYH 758
                                       TNRNVNPDGSLIANGY ----NWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIEN 603
                                                                                                                                                     .-----VRI 203
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Sequence 200, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COMMENDER.
                                                                       129 TORPOFVDLDRVRVEYFNAKENINSFLRKOSACNII---FRTAIVRAHHIR--FNENLNT
                                                                                                               604 AVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINY
                                                                                                                                                                                           ----YDKFDDLDESRKYIFNKTAEYQEEMDML-KDLKLIQNKDAKIAVSIFY-
                                                                                                                                                                                                                                                                                                    242 AIKRATNPKVREFIVTKMGNKIANEFEPTRYDIN-----ERYQTHKDTLVELSKFLH
                                                                                                                                                                                                                                                                                                                                            759 KHQVN-----NKLSQL-----ILLNNDI-SYYTSNRLIKTEAHLSNI-----NKLSQL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER EABDABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP VECTER 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                        795 -NLNCEYIIFDNHDSLFVKNDS----YAYMKKY----
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                                                                                                                                           NAME: BLOOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 200: SEQUENCE CHARACTERISTICS:
LENGTH: 674 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603 NAVDYDMFLKLSEVGKFKHLNKICY-NRVLHGD---------NTSIKKL 641
                                                                                                                                                                                                                                                                                                                                                                                                                                   642 GIQKKNHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQN 701
                                                                                                                                                    451 CVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMSKPNGGIASASNAAVSF 510
                                                                                                                                                                                                                                            -VNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHL------TDGFNENIE 602
                                                                                                                                                                                                                                                                                                                      227 GYPLEKHLAVYROMLEVSLAN----GOASGLSDTATY----KEFEMKORLLNQLSROEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GOLSChlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                                    115;
                                                                               Length 674;
                                                                                                                    Indels
                                                                                                                                                                                                                            511 AKGYYIGQLDSDDYLEPDAVELCLK---EFLKDKTLACVYTTNRN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,387B
FILING DATE: July 7, 1994
CLASSIFICATION: 435
                                                                               Query Match

4.4%; Score 223.5; DB 4;
Best Local Similarity 20.1%; Pred. No. 7.8e-11;
Matches 96; Conservative 89; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CIIY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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                                 , MOLECULE TYPE: protein US-08-961-083-200
STRANDEDNESS: single
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                    linear
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Gaps

48;

Length 348;

us-09-842-484a-2.rai

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                                                                                                                                                   433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                                                                                                                                                                                       493 MSK-PNGGIASASNAAV-SFAK----GYYIGQLDSDDYLEPDAVELCLKEFLKDKTLAC 545
                                                                                                                                                                                                                                                                546 V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI-----AHHFRMFTIRAWHLT 594
                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF TITLE OF INVENTION: GLIGOSACCHARIDES, AND GENES ENCODING THEM NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     644 QK--KNHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQ-EEMDM 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 QKTARNDFL---QSMGFK-----TRFDSLE---YRQTKAAAYELPEKDL 278
                                                               Query Match 4.1%; Score 210; DB 1; Length 348 Best Local Similarity 26.4%; Pred. No. 4.1e-10; Matches 77; Conservative 57; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUTE. 7.001

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08683426 Patent No. 5705367
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411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 201343-1684
TELEX: 133521
INFORMATION FOR SEQUENCE CHARACTERISTICS:
FENDENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 348 amino acids
amino acid
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; MOLECULE TYPE: protein US-08-312-387B-11
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New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                   546 V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI-----AHHFRMFTIRAWHLT 594
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                                                                                                                                                                                                                                                                                                    433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                               3 PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08312387B
Patent No. 554553
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 QKTARNDFL---QSMGFK-----TRFDSLE----YRQTKAAAYELPEKDL 278
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                                                                                                                                                                                                                   Length 348;
                                                                                                                                                                                                                4.1%; Score 210; DB 1; Length 346
26.4%; Pred. No. 4.1e-10;
tive 57; Mismatches 110; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,387B
FILING DATE: July 7, 1994
CLASSIFICATION: 435
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CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORREY/AGRY INFORMATION:
NAME: Jackson Esq., David A.
REGISCHATION NUBBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 411 Hackensack Avenue
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
               TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                           77; Conservative
201 343-1684
                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-312-3878-3
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
21P: 07601
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Best Local Similarity
Matches 77; Conserva
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TELEFAX:
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COUNTRY:
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                                                                                                                          493 MSK-PNGGIASASNAAV-SFAK----GYYIGQLDSDDYLEPDAVELCLKEFLKDKTLAC 545
                                                                                                                                            546 V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI-----AHHFRMFTIRAWHLT 594
                                                                                                                                                                                                           433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                 Gaps
                                                                               DG---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK------KLGI
                                                                                                                                                                                                                                                                                   181 DGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQGI
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4.18; Score 210; DB 1; Length 348;
Best Local Similarity 26.4%; Pred. No. 4.1e-10;
Matches 77; Conservative 57; Mismatches 110; Indels
   DB 1; Length 348;
Query Match
4.1%; Score 210; DB 1; Length 348
Best Local Similarity 26.4%; Pred. No. 4.1e-10;
Matches 77; Conservative 57; Mismatches 110; Indels
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PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERBENCE/DOCKET NUMBER: 600-1-095B
TELECOMMUNICATION INFORMATION:
TELECHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/683,426
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                      193 MSK-PNGGIASASNAAV-SFAK----GYYIGQLDSDDYLEPDAVELCLKEFLKDKTLAC 545
546 V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI----AHHFRMFTIRAWHLT
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Sequence 3, Application US/08683458
Sequence 3, Application US/08683458
Patent No. 579823
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              644 QK--KNHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQ-EEMDM 692
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4.1%; Score 210; DB 1; Length 348
Best Local Similarity 26.4%; Pred. No. 4.1e-10;
Matches 77; Conservative 57; Mismatches 110; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 435
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ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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STREET: 411 Hackensack Avenue
CITY: Hackensack
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TELEFAX: 201 343-1684
TELEX: 13351
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
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493 MSK-PNGGIASASNAAV-SFAK----GYYIGQLDSDDYLEPDAVELCLKEFLKDKTLAC 545 ::: | | : : | | : : | | | :::
  433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
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                                                                        546 V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI-----AHHFRMFTIRAWHLT
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APPLICANT: Gotschlich, Emil C.
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLFRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     644 QK - KNHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQ-EEMDM 692
                                                                                                                                                                                                                                                                                                241 QKTARNDFL---QSMGFK-----TRFDSLE----YRQTKAAAYELPEKDL 278
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COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,360
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
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FILING DATE: September 26, 1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1 TELECOMMUNICATION INFORMATION: TELEFHONE: 201 487-5800 TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08878360 Patent No. 5945322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-878-360-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                               181 DGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQGI 240
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                                               493 MSK-PNGGIASASNAAV-SFAK-----GYYIGQLDSDDYLEPDAVELCLKEFLKDKTLAC 545
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                                                                                            63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                            546 V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI-----AHHFRMFTIRAWHLT 594
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3 PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                                                                                                                                                                         DG---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK-----KLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       241 QKTARNDFL---QSMGFK-----TRFDSLE----YRQTKAAAYELPEKDL 278
                                                                                                                                                                                                                                                                                                                                      644 QK--KNHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQ-EEMDM 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LICATION DATA:
TON NUMBER: 08/312,387
DATE: September 26, 1994
IGATION: 435
ACENT INFORMATION:
Jackson Esq., David A.
ATTON NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/683,458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08683458 Patent No. 5798233
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TELECOMMUNIQATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 77; Conserve
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PRIOR APPLI
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POLYGLYCOSYLTRANSFERASE, A
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                                                                                                                    181 DGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANOVSSKHSVRQHEIAQGI 240
                                     123 MGAWLEVLSEEKDGNRLARHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRS--VI 180
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      ---NGYNWPEFSREKLTTAMI-----AHHFRMFTIRAWHLT
                                                                                                                                                                                                                                                                                                                                                                                                                       METHOD OF TRANSFERRING AT LEAST TWO SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFER POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A POLYGLYCOSYLTRANSFERASE
                                                                                                                                                               644 QK--KNHFVVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQ-EEMDM 692
                                                                                                                                                                                        Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,140B FILING DATE: US/01/1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         core 210; DB 3;
red. No. 4.1e-10;
Mismatches 110;
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26.4%; Pred. No. 4
:ive 57; Mismatch
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08478140B Patent No. 6127153
GENERAL INFORMATION:
APPLICANT: JOHNSON, KARL F.
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: JOHNSON, KARL F.
APPLICANT: ROTH, STEPHEN
APPLICANT: BUCZALA, STEPHANIE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Laura A. COTUZZI
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7188
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (212) 790-9090
(212) 869-9741/8864
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 26.4
Matches 77; Conservative
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; MOLECULE TYPE: protein
US-08-478-140B-3
              546 V -- YTTNRNVNPDGSLIA-
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COUNTRY: USA
ZIP: 10036-2711
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US-08-478-140B-3
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                                                                                                                                                 63 LAQAQNSGLIPSLNIGLDELAKSGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                     546 V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI-----AHHFRMFTIRAWHLT 594
                                                                                                                  595 DG---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK-----KLGI
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GOLSCHlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                               644 QK--KNHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQ-EEMDM 692
                                                                                                                                                                                                                        241 QKTARNDFL---QSMGFK-----TRFDSLE----YRQTKAAAYELPEKDL 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.1%; Score 210; DB 2; L
26.4%; Pred. No. 4.1e-10;
1ve 57; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: September 26, 1994
CLASSIFICATION: 435
ATONINEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERRENCE/POCKET NUMBER: 600-1-09:
TELECOMMUNICATION INFORMATION:
TELECPHONE: 201 487-5900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 133521
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 26.48
Matches 77; Conservative
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APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackenser
STATE: New Jersey
COUNTRY: USA
7.IP: 07601
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US-08-878-360-11
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GenCore version 5.1.3
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OM protein - protein search, using sw model

January 4, 2003, 02:26:45; Search time 203 Seconds Run on:

(without alignments) 90.090 Million cell updates/sec

US-09-842-484A-2 5089 1 MNTLSQAIKAYNSNDYELAL.....SAKKGENIPVNKFIINSITL 965 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Sequence:

Scoring table:

117078 seqs, 18951520 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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// Cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
// Cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
// Cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:* Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result No.	Score	Query Match	Juery Aatch Length DB	DB	ΩI	Description
-	7 7877		07.5		110-00-070-060-10	
+	7.00	7.00	716	ת	07_666_6/9_60_60	sednence In' Appi
7	276.5	5.4	206	10	US-09-815-242-4950	Sequence 4950, Ap
m	276.5	5.4	715	10	US-09-815-242-10511	
4	246	4.8	322	10	US-09-767-041-34	
S	224	4.4	332	10	US-09-767-041-22	Sequence 22, Appl
9	223.5	4.4	278	10	US-09-767-041-36	Sequence 36, Appl
7	223.5	4.4	674	10	US-09-765-272-200	Sequence 200, App
8	217.5	4.3	332	10	US-09-767-041-21	Sequence 21, Appl
6	210	4.1	348	12	US-10-007-267-3	Sequence 3, Appli
10	210	4.1	348	12	US-10-007-267-11	Ξ
11	209	4.1	337	12	US-10-007-267-5	5, 4
12	209	4.1	337	12	US-10-007-267-12	12
13	208.5	4.1	270	10	US-09-816-028A-39	39,
14	207	4.1	301	10	US-09-816-028A-27	27,
15	202	4.0	389	10	US-09-816-028A-34	34,
16	200.5	3.9	303	10	US-09-816-028A-29	29,
17	199	3.9	297	10	US-09-816-028A-31	Sequence 31, Appl
18	194	3.8	120	10	US-09-767-041-52	
19	194	3.8	322	10	US-09-767-041-35	Sequence 35, Appl

Sequence 51, Appl Sequence 29, Appl Sequence 3905, App Sequence 196, App Sequence 196, Appl Sequence 198, Appl Sequence 1, Appl Sequence 1, Appl Sequence 202, Appl Sequence 202, Appl Sequence 26, Appl Sequence 29, Appl Sequence 4, Appl Sequence 4, Appl Sequence 498, A	Sequence 8, Appli
10 US-09-767-041-51 10 US-09-924-358-29 9 US-09-738-626-3905 9 US-09-738-626-3905 10 US-09-765-272-198 10 US-09-765-272-198 10 US-09-96-272-198 10 US-09-916-028A-33 10 US-09-816-028A-33 10 US-09-816-028A-33 10 US-09-816-228-25714 10 US-09-815-228-25714 10 US-09-815-228-25714 10 US-09-815-228-25714 10 US-09-815-228-25714 10 US-09-815-228-25714 10 US-09-815-228-25714 10 US-09-815-228-257-4 10 US-09-816-288-354-98 10 US-09-978-657-4 12 US-10-074-527-4 13 US-10-074-527-4 14 US-10-074-527-4 15 US-10-074-527-4 16 US-09-978-697-498 17 US-09-978-697-498 18 US-09-978-697-498 18 US-09-978-697-498 18 US-09-978-697-498 18 US-09-978-697-498	9 US-09-843-676-8
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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Weigel, Paul H
APPLICANT: Kumart, Kshama
APPLICANT: Kumart, Kshama
APPLICANT: To Edul H
APPLICANT: To Edul H
APPLICANT: To Edul H
APPLICANT: Deangelis, Paul H
TITLE OF INVENTION: STREPTOCCCCUS EQUISIMILIS HYALURONAN SYNTHASE GENE AND EXPRESS
TITLE OF INVENTION: IN BACILLUS SUBTILIS
FILE REFERENCE: 3554.049
CURRENT APPLICATION NUMBER: US/09/879,959
CURRENT FILING DATE: 1090-102
PRIOR FILING DATE: 1999-12-21
PRIOR PLICATION NUMBER: 09/469,200
PRIOR FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KEEKVNVCDSPLDIATQLLLSNVKKLVLSDSEKNTLKNKWKLLTEKKSENAEVRAVALVP 120
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                     Sequence 10, Application US/09879959 Patent No. US20020160489A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: pasteurella multocida US-09-879-959-10
US-09-879-959-10
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LENGTH: 972
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174 VNQKTNYPFEVVVADDGSKENLLTIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKY 233

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                                                                               101 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRLSDSPFRFFAAGNVAFAKKWLNKSGFFD
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DFVSILDCDMAPQQLWVHSYLTELEDNDIVLIGPRKYVDTHNITAEQFLNDPYLIESLP
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JOHERANI LINGUARATION:
JOHERANI LINGUARATION:
JOHERANI ZYSKING, JUGITH W.
JOHERANI: ZYSKING, JUGITH W.
JOHERANI: Trawick, John D.
JOHERANI: Trawick, John D.
JOHERANI: Carr, Grant J.
JOHERANI: Carr, Grant J.
JOHERANI: Xu, H. HOWARD
JITLE OF INVENTION: Identification of Essent:
JITLE OF INVENTION: PROMARYOTES
JITLE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 4950, Application US/09815242; Patent No. US20020061569A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKE 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 DNDIVLIGPRKYVD--THNITAEQFLNDPYLIESLPETATNNNPSITSKGNISLDWR--- 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 706;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.4%; Score 276.5; DB 10; Best Local Similarity 21.5%; Pred. No. 1.2e-12; Matches 151; Conservative 115; Mismatches 268;
                                                                                                                                                                                                                                                                                                                                                                                                     4.0
          PRIOR APPLICATION UNBER: 60/191,078
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-2
PRIOR FILING DATE: 2000-12-2
PRIOR PILING DATE: 2000-12-2
PRIOR PILING DATE: 2001-12-2
PRIOR PILING DATE: 2001-12-2
PRIOR PILING DATE: 2001-12-2
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRISES FOR WINDOWS VERSION 4.CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecalis
2001-03-21
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LENGTH: 706
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Sequence 34, Application US/09767041
; Sequence 34, Application US/09767041
; Patent No. US20020055168A1
; GENERAL INFORMATION:
    APPLICAMT: Smith, Hilda
; TITLE OF INVENTION: 2183-4726
    CURRENT APPLICATION NUMBER: US/09/767,041
    CURRENT PELICATION NUMBER: PCT/NL99/00460
; PRIOR PLICATION NUMBER: PCT/NL99/00460
; PRIOR FILING DATE: 1999-07-19
; PRIOR PLILOR DATE: 1998-07-2
; PRIOR APPLICATION NUMBER: EP98202465.5
; PRIOR PLILOR DATE: 1998-07-2
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                   ENWLTLMVSFAQQERIGCVGAKLLYPNNTVQHAGVILGLGGVAGHGHYGYPHGDLGYFGR 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 LVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIM 493
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    341 ILEEIGGFRKGYEGSQDYDLVLRFTERTTKERITHIPKVLYYWRMLPTSTAVDQGSKGYA 400
                                                                                                                                                                                                                                       697 KLIQNKDAKIAVSIFYPNTLNG---LVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEI 753
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                                                                                                                                         401 FEAGLRAVQDALVRRGINGHATHGAANGLYDVYYDI-ESEK----
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4.8%; Score 246; DB 10;
Best Local Similarity 25.3%; Pred. No. 7e-11;
Matches 92; Conservative 58; Mismatches 120;
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OTHER INFORMATION: CPS11
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US-09-767-041-34
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LENGTH: 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKVTRLW------IKAKKGFKYMAKNGIS-HTIQRAKIEKLRNQA--SYLNWLARN 163
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APPLICANT: 2yskind, Judith W.
APPLICANT: 2yskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Carry Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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    LAINVNYSAVTAACLLMKKADFDAVGGFEEAFTVAFNDVDL 637
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CURRENT FILING DATE: 2001-03-21
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-3
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10511
LENGTH: 715
                                                                                                                                                                                          ce 10511, Application US/09815242
No. US20020061569A1
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US-09-815-242-10511
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
597
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         605 VDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINYY 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       665 NYDKFDDLDES--RKYIFNKTAEYQ-EEMDML-----KDLKLIQNKDAKIAVSIF----Y 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 YVDRENSIITSSMTDHRFHCLLEFQNERMDFYESRGDKEL-LLECYRSFLAFAVLFLGKY 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----NVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIENA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 SCHFLTAEPLPTNQAVLSGRN----VCKKLLEA-DGHRF----VVAWN------KL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNR--- 551
708 VSIFYPNTLNGLVKKLNNIIEYN--KNIFVIILHVDKNHLT--PDIK-KEILAFYHKHQV 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS
                          Sequence 22, Application US/09767041
Patent No. US20020055168A1
GENERAL INFORMATION:
APPLICANT: Smith, Hilda
TITLE OF INVENTION: STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS
FILE REFERENCE: 2183-4726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.4%; Score 224; DB 10; Length 332; ilarity 24.4%; Pred. No. 3.1e-09; Conservative 65; Mismatches 118; Indels 6
                                                                                                                                                                                                                                                                                                                                 FILE KEPEARANE: 4.103 4/20

CURRENT PELLING DATE: 2001-01-22

PRIOR APPLICATION NUMBER: US/09/767,041

PRIOR FILING DATE: 1999-07-19

PRIOR APLICATION NUMBER: EP98202465.5

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin Version 3.0

SOFTWARE: Patentin Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Streptococcus suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; OTHER INFORMATION: CPS2K
US-09-767-041-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Smith, Hilda
TITLE OF INVENTION: ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                            255 -----
                                                                               763 NILL 766
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301 TLYL 304
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US-09-767-041-36
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Matches
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Sequence 200, Application US/09765272
Sequence 200, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
APPLICANT: Choi et. al.
APPLICANT: Choi et. al.
NUMBER OF EQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 YFKKENGGLSDARNYGISRAKGDYLAFIDSDDFIHSEFIQRLHEAIERENALVAVAGYDR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               432 IPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVR 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ISKISIIVPIYNVEKYLSKCIDSIVNQTYKHIEILLLVNDGSTDNSEEICLAYAKKDSRIR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.4%; Score 223.5; DB 1 Best Local Similarity 34.1%; Pred. No. 2.7e-09; Matches 44; Conservative 29; Mismatches 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB340P2
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 200:
CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/00460
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 53
SSOFUR NOS: Patentin version 3.0
LENGTH: 278
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APPLICATION WUMBER: 08/961,083
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                        PCT/NL99/00460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Scier
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptococcus suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KET: misc_feature
; OTHER INFORMATION: CPS1K
US-09-767-041-36
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                                                                                                                                                                                                                                                                                                                                                  NVNPDGSLIAN-GYNWPEFSREK-----IR 589
                                                                                                                                                                                                                       495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVE---LCLKEFLKDKTLACVYTTNR 551
                                                                                                435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                         Gaps
                                                                                                                                          4 VSIIVPIFNTEKYLRECLDSIISQSYTNLEILLIDDGSSDSSTDICLEYAEQDGRIKLFR 63
                                                                                                                                                                                                                                                              64 LPNGGVSNARNYGIKNSTANYIMFVDSDDIVDGNIVESLYTCLKE--NDSDLS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10007267
Patent No. US20020127682A1
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
APPLICANT: GOTSCHlich, Emil C.
APPLICANT: GOTSCHLICH, GOTSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 680 FNKTAEYQEEMDML--KDLKLIQNKDAKIAVSIFYPNTLNGLVK-KLNNIIEYNKN 732
                                   87;
                                      Indels
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24.2%; Prec. w...
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APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Unn-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/007,267
FILING DATE: 03-Dec-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 348 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FELEFAX: 201 343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
COUNTRY: USA
      Best Local Similarity 24.29
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PELEX: 133521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -VNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHL-----TDGFNENIE 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 --LNOKVYL-LSE--KVIYLNKSLYAYRIRKGSLSRVWTEKWMHALVDAMSERITLLANM 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            642 GIQKKNHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQN 701
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278 SEKKAIVLAANYGYVDQVLTTIKSICYHNRSIRFYLIHSDFPNEWIKQLNKRLEKFDSEI 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYPLEKHLAVYROMLEVSLAN----GOASGLSDTATY----KEFEMKORLLNOLSROEE 277
                                                                                                                                                                                                                                                                                                                                                                                                               V: STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS
2183-4726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : |: | :: | :| :| :| DLQDYPLAAVRDFGGRAYFGQEIFNAGVLLVNNAFWKKENMTQKLIDVTNEWHDKVD 449
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                                                                                                                                                                                                                                                                                                                  Indels 115;
                                                                                                                                                                                                                                                        Length 674;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      511 AKGYYIGQLDSDDYLEPDAVELCLK---EFLKDKTLACVYTTNRN-----
                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                 4.4%; Score 223.5; DB 10; 20.1%; Pred. No. 9.1e-09; tive 89; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAVDYDMFLKLSEVGKFKHLNKICY-NRVLHGD----
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Patent No. US2002005516841
GENERAL INFORMATION:
APPLICANT: Smith, Hilda
TITLE OF INVENTION: STREPTOCOCCUS SUIS VAC;
FILE REFERENCE: 2183.4726
CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: EP98202465.5
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1998-07-22
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SSOFTWARE: Patentin version 3.0
                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 200:
US-09-765-272-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999-07-19
   LENGTH: 674 amino acids
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                                                                                                                                                                                                                                                                                                              Conservative
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OTHER INFORMATION: CPS2J
                                                                                                                                                                                                                                                                              Local Similarity
les 96; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-767-041-21
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RESULT 11
US-10-007-267-5
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                                                                                                                                                                                                          433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                        Gaps
                                                                                                                             546 V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI-----AHHFRMFTIRAWHLT
                                                                                                                                                                                                                                                                                                                                   DG---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK------KLGI
                                                                                                                                                                                                                                                                                                                                                                     181 DGGLRYDTERDWAEDYQFWYDVSKLGRLAYYPEALVKYRLHANQVSSKHSVRQHEIAQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                                        48;
                                                                                                                                                                                                                                                                                                                                                                                                                                 241 QKTARNDFL---QSMGFK-----TRFDSLE----YRQTKAAAYELPEKDL 278
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                                   Length 348;
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DAYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/007,267
FILING DATE: 03-D02-2001
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: 17-Jun-1999
APPLICATION NUMBER: 08/312,387
                               Score 210; DB 12;
Pred. No. 3.6e-08;
                                                                      57; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein SEQ ID NO: 11: US-10-007-267-11
                                 4.1%; Score 210; 26.4%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gotschlich, Emil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/10007267
Patent No. US20020127682A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 348 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201 343-1684
TELEX: 133521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New Jersey
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                                 Query Match
Best Local Similarity 26.45
Matches 77; Conservative
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US-10-007-267-3
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                                                                                                                                                                                                                              63 LAQAQNSGLIPSLNIGLDELAKSGGGGGEYIARTDADDIASPGWIEKIVGEMEKDRSIIA 122
                                                                                                                                                                                                                                                                                                                               123 MGAWLEVLSEEKDGNRLARHHKHGKIWKKPTRHEDIAAFFPFGNPIHNNTMIMRRS--VI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                     433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                                                                                                                                                                                                                                               546 V--YTTNRNVNPDGSLIA----NGYNWPEFSREKLTTAMI----AHHFRMFTIRAWHLT 594
                                                 Gaps
                                                                                                                                             3 PLVSVLICAYNVEKYFAQSLAAVVNQTWRNLDILIVDDGSTDGTLAIAKDFQKRDSRIKI 62
                                                                                                                                                                                                                                                                                                                                                                                                     595 DG---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK-----KLGI
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TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
OLIGOSACCHARIDES, AND GENES ENCODING THEM
                                                 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 QKTARNDFL---QSMGFK-----TRFDSLE----YRQTKAAAYELPEKDL 278
  Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      644 QK--KNHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQ-EEMDM
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
4.1%; Score 210; DB 12;
26.4%; Pred. No. 3.6e-08;
Live 57; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/007,267
FILING DATE: 03-Dec-2001
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Un-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: JUJy 7, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1-095
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-007-267-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/10007267 Patent No. US20020127682A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201 343-1684
TELEX: 133521
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COMPUTER READABLE FORM:
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COUNTRY: USA
                               Best Local Similarity 26.4%
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Hackensack
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639

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Sequence 39, Application US/09816028A

Sequence 39, Application US/09816028A

Patent No. US20020042369A1

GENERAL INFORMATION:

APPLICANT: Glibert, Michel

APPLICANT: National Research Council of Canada

TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of

TITLE OF INVENTION: Campylobacter Glycosyltransferases

CURRENT PRILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/118,213

PRIOR FILING DATE: 1999-02-01

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 49

SEGTWARE PATENTION OF 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                           ----VYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMI-----AHHFRMFTIRAWHLTDG 596
                                                                                                                                                                                                                                                                                                                                                 61 IFQNEENLGTFASRNLGVLHSSSDFIMFLDSDDFLTPDACEIAFKEMKKGFDLLCF---- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 RNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENI-ENAVDYDM 609
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                                                                                                                                                 433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: glycosyltransferase from C. jejuni OH4384 (ORF 12a; OTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus) US-09-816-028A-39
                                                                                                                                                                                                                                                                                                                                                                                                              ---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KLGIQKKNHFVVVNQSLNRQGI----NYYNYDKFDDLDESRK
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                                                                                                           Indels
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4.1%; Score 208.5; DB 10;
Best Local Similarity 23.7%; Pred. No. 3.3e-08;
Matches 78; Conservative 54; Mismatches 122;
                                                                                                         53; Mismatches 129;
                                                              ; DB 12;
4.1e-08;
                                                            Score 209;
Pred. No. 4.
  SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Campylobacter jejuni
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                                                                                                         Conservative
                                                                Query Match
Best Local Similarity
Matches 75; Conserv
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                    US-10-007-267-12
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LENGTH: 270
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                                                                                                                                                                                                                                                                                       123 AWLEVLSEENNKSVLAAIARNGAIWDKPTRHEDIVAVFPFGNPIHNNTMIMRRS--VIDG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 EIRAGYWKAAGIAVGADCLNYGLLKSTAYALYEKALSGQDIGCLRLFLYEYFLSLE---K 297
                                                                                  433 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                              Gaps
                                                                                                             -----NYYNYDKEDDLDESRK
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Patent No. US20020127682A1
GENERAL INFORMATION:
GAPPLICANT: GGISCHILCH, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
OLIGOSACCHARIDES, AND GENES ENCODING THEM
  Length 337;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                               ---FNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIK----
4.1%; Score 209; DB 12;
23.7%; Pred. No. 4.1e-08;
tive 53; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHORE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/007,267
TLING DATE: 03-Dec-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 337 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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                                          75; Conservative
                      Similarity
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US-10-007-267-12
Query Match
                      Best Loc
Matches
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Patent No. US20020043369A1

GENERAL INFORMATION:

APPLICANT: Gilbert, Michel

APPLICANT: Waxarchuk, Warren W.

APPLICANT: Waxarchuk, Warren W.

APPLICANT: National Research Council of Canada

TITLE OF INVENTION: Canapiloasdes and Ganglioside Mimics

TITLE OF INVENTION: Gangliosides and Ganglioside Mimics

FILE REFERENCE: 019633-000111US

CURRENT APPLICATION NUMBER: US 60/118,213

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 1999-02-01

PRIOR APPLICATION NUMBER: US 60/118,213

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 49

SOFTWARE PATENT VAIL VAIL SOFT SEQ ID NOS: 49

SEQ ID NO 27

LENGTH NO 27

LENGTH NO 27

LENGTH NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
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US-09-816-028A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 612
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                                                                                                                                                                                                                                                    664 YNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFY-PNTLNGLVKK 722
                                                                                                                                                                                                                                                                                                                           --ENKNKEILNONYHDKKKSNEIIKK 240
610 FLKLSEVGKF-KHLN----KICYNRVLHGDNTSIKKLGIQKKNHFVVVVNQSLNRQGINY 663
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4.1%; Score 207; DB 10; Length 301;
Best Local Similarity 21.0%; Pred. No. 4.9e-08;
Matches 78; Conservative 64; Mismatches 116; Indels 114;
                                                                                                                                                                            166 ILKSFEKIKIDERLNYGEDVLFCYIYFMFCEKIAVFKTCI--
                                                                                                                                                                                                                                                                                                         723 LNNII---EYNKNIFVIILHVD---KNHL 745
                                                                                                                                                                                                                                                                                                                                                                                                                                            |::::|::|241 LSKEFAHDEFHQKLFEVLKREEAGVKNRL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Campylobacter jejuni
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US-09-816-028A-27
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Squence 34, Application US/09816028A

Squence 34, Application US/09816028A

Patent No. US20020043369A1

GENERAL INFORMATION:
APPLICANT: Glibert, Michel

APPLICANT: National Research Council of Canada

TITLE OF INVENTION: Canapliosater Glycosyltransferases for Biosynthesis of

TITLE OF INVENTION: Gangliosides and Ganglioside Mimics

TITLE OF INVENTION: Gangliosides and Ganglioside Mimics

CURRENT PRILICATION NUMBER: US/09/816,028A

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/118,213

PRIOR FILING DATE: 1999-02-01

PRIOR PELING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 49

SGFWARRE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LSQKLYLCRLRANS----ISNHD-----KK------TTKAN 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VITALKLIEFFKD 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KFDDLDESRKYIFNKTAEYQEEM-DMLKDLKLIQNKDAKIAVSIFYPNTLNGLVKKLNN 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDIS-----YYTSNRLIK 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: glycosyltransferase of C. jejuni OH4384 (ORF 4a of OTHER INFORMATION: lipooligosaccharide (LOS) biosynthesis locus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         900 YNTEDIWFQFALLILEKKTGHVFNKTSTLTYMPWERKLQWTNEQIQSAKKGENIPVN 956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 21.2%; Pred. No. 9.9e-08;
Matches 114; Conservative 81; Mismatches 146;
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ORGANISM: Campylobacter jejuni
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Search completed: January 4, 2003, 02:49:25 Job time: 206 secs

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January 4, 2003, 02:23:10 ; Search time 400 Seconds (without alignments) 1555.419 Million cell updates/sec
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	Description		Sequence 2, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 8, Appli	Sequence 3, Appli
SUMMARIES	Ę		PCT-US01-13395-2	PCT-US99-26501-3	PCT-US01-13395-4	PCT-US99-07289-3	PCT-US99-07289-8	US-09-283-402-3
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ALIGNMENTS

RESULT 1 PCT-US01-13395-2

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Sequence 2. Application PC/TUS0113395
GENERAL INFORMATION:
APPLICAMT: DE ANGELIS, PAUL L.
TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND TITLE OF INVENTION: USING SAME
FILE REPERENCE: 618755-9/JP/199, 538
CURRENT APPLICATION NUMBER: PCT/US01/13395
CURRENT FILING DATE: 2001-04-25
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PALENTING DATE: 2000-04-25
LENGTH: 965
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ORGANISM: Pasteurella multocida
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Matches 965; Conservative
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                                                   CDMAPQQLWVHSYLTELLEDNDIVLIGPRKYVDTHNITAEQFLNDPYLIESLPETATNNN
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      CDSSLHIATQLLLSNVKKLTLSESEKNSLKNKWKSITGKKSENAEIRKVELVPKDFPKDL
                            VLAPLPDHVNDFTWYKNRKKSLGIKPVNKNIGLSIIIPTFNRSRILDITLACLVNQKTNY
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GENERAL INFORMATION:
APPLICANT: THE BOARD OF REGENTS OF THE UNIVERSITY OF OKLAHOMA
TITLE OF INVENTION: POLYMER GRAFTING BY POLYSACCHARIDE SYNTHASES
FILE REFERENCE: 617481-5
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Conservative 0; Mismatches
  APPLICATION NUMBER: PCT/US99/26501
CURRENT APPLICATION NUMBER: FC1,CC2,CCGRRENT FILING DATE: 1999-11-10
EARLIER APPLICATION NUMBER: 60/107,929
EARLIER FILING DATE: 1998-11-11
EARLIER FILING DATE: 1999-04-01
EARLIER FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 965
                                                                                                                ORGANISM: Pasteurella multocida
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Matches 965; Conserv
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                                                                                                                                               Match
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Sequence 3. Application PC/TUS9907289
GENERAL INFORMATION:
APPLICANT: Board of Regents of the University of Oklahoma
TITLE OF INVENTION: UNCLEIC ACID ENCODING HYALURONAN SYNTHASE AND METHODS
TITLE OF INVENTION: OF USE
FILE REFERENCE: 617022-7
CURRENT APPLICATION NUBBER: CT/US99/07289
CURRENT FILING DATE: 1999-04-01
EARLIER APPLICATION NUBBER: 60/080,414
EARLIER PILING DATE: 1998-04-02
EARLIER FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN OF: 2.0
                                                                                                                                                                                                                                                                                                                                                             TEAHLSNINKLSQLNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGMNFSALTHDWIEKIN 840
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TITLE OF INVENTION: CHONDROITIN SYNTHASE GENE AND METHODS OF MAKING AND TITLE OF INVENTION: USING SAME
FILLE REFERENCE: 618755-9/JD/199,538
CURRENT APPLICATION NUMBER: PCT/US01/13395
CURRENT APPLICATION NUMBER: PCT/US01/13395
CURRENT APPLICATION NUMBER: 09/437,277
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR FILING DATE: 1099-11-10
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SSOFTWARE: Patentin Ver. 2.1
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99.6%; Score 5067;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 960; Conservative 2; Mismatches
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ORGANISM: Pasteurella multocida
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; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Oklahoma
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HYALURONAN SYNTHASE AND
; TITLE OF INVENTION: OF USE
; FILE REFERENCE: 617022-7
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: 60/080,414
; EARLIER APPLICATION NUMBER: 60/080,414
; EARLIER PILING DATE: 1998-04-02
; EARLIER FILING DATE: 1998-04-02
; EARLIER FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
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                                             Score 5017.5;
Pred. No. 0;
5; Mismatches
                           multocida (PmCS)
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                                               98.6%;
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3; Conservative
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hes 953;
SOFTWARE: Pate
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                   TYPE: PRT
ORGANISM: 1
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901 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSTLTYMPWERKLOWTNEOIOSAKKGENI 960
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                                                                 US-09-283-402-3

Sequence 3, Application US/09283402

Sequence 3, Application US/09283402

GENERAL INFORMATION:

APPLICANT: Paul Deangel1s

TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA

TITLE OF INVENTION: MULTOCIDA AND USES THEREOF

FILE REFERENCE: 5820.530

CURRENT APPLICATION NUMBER: US/09/283,402

CURRENT FILIC DATE: 1999-04-01

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                           LKEFLKDKTLACVYTTNRNVNDDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHL
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Pred. No. 0;
5; Mismatches
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; ORGANISM: Pasteurella multocida
US-09-283-402-3
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98.0%;
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Best Local Similarity 98.0
Matches 953; Conservative
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Sequence 8, Application US/09283402

Sequence 8, Application US/09283402

GENERAL INFORMATION:

APPLICANT: Paul Deangelis

TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA

TITLE OF INVENTION: MULTOCIDA AND USES THEREOF

FILE REFERENCE: 5820.530

CURRENT APPLICATION UNDER: US/09/283,402

CURRENT FILING DATE: 1999-04-01

NUMBER OF SEO ID NOS: 29 IDSVPEYNTEDIWFQFALLILEKKTGHVFNKTSTLTYMPWERKLQWTNEQIQSAKKGENI 1 MNTLSQAIKAYNSNDYELALKLFEKSAETYGRKIVEFQIIKCKEKLST-----NSYVS KDFPKDLVLAPLPDHVNDFTWYKNRKKSLGIKPVNKNIGLSIIIPTFNRSRILDITLACL VNQKTNYPFEVVVADDGSKENLLTIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKY NTLNGLVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYY DB 16; Length 972; Indels ′,

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                    DNTLEWINKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELC
                                                          EEFNHWGGEDVEFGYRLFPKGCFFRVIDGGMAYHQEPPGKENETEREAGKSITLKIVKEK
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GENERAL INFORMATION:
APPLICANT: Board of Regents of the University of Oklahoma
TITLE OF INVENTION: NUCLEIC ACID ENCODING HYALURONAN SYNTHASE AND
TITLE OF INVENTION: OF USE
FILE REFERENCE: 617022-7
CURRENT APPLICATION NUMBER: US/09/469,200
CURRENT PELING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/080,414
PRIOR PILING DATE: 1998-10-26
PRIOR FILING DATE: 1999-10-26
NUMBER OF SEQ IN NOS: 29
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Pred. No. 0;
5; Mismatches
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ORGANISM: Pasteurella multocida
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llarity 98.0%;
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SEQ ID NO 3
LENGTH: 972
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Sequence 8, Application US/09469200
GENERAL INFORMATION:
APPLICANT: Board of Regents of the University of Oklahoma
TITLE OF INVENTION: NUCLEIC ACID ENCODING HYALURONAN SYNTHASE AND METHODS
TITLE OF INVENTION: OF USE
FILE REFERENCE: 617022-7
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                              KDFPKDLVLAPLPDHVNDFTWYKNRKKSLGIKPVNKNIGLSIIIPTFNRSRILDITLACL
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Sequence 9, Application PC/TUS9907289

Sequence 9, Application PC/TUS9907289

GENERAL INFORMATION:
APPLICANT: Board of Regents of the University of Oklahoma
TITLE OF INVENTION: NUCLEIC ACID ENCODING HYALURONAN SYNTHASE AND METHODS
TITLE OF INVENTION: NUCLEIC ACID ENCODING HYALURONAN SYNTHASE AND METHODS
TITLE OF INVENTION: OF USE
FURENT PELICATION NUMBER: PCT/US99/07289
CURRENT FILING DATE: 1999-04-01
EARLIER PPLICATION NUMBER: 60/080,414
EARLIER FILING DATE: 1998-04-02
EARLIER FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VET. 2.0
SOFTWARE: PATENTIN VET. 2.0
                                                                                                   DWIEKINAHPPFKKLIKTYFNDNDLRSMNVKGASQGMFMKYALPHELLTIIKEVITSCQS
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CURRENT APPLICATION NUMBER: US/09/469,200
CURRENT FILING DATE: 1999-12-21
FINEN APPLICATION NUMBER: 60/080,414
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 60/178,851
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver: 2.0
SEQ ID NOS 2
                                                                                                                                                               TYPE: PRT ORGANISM: Pasteurella multocida (PmCS)
                                                                                                                                                                                           US-09-469-200-8
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KDFPKDLVLAPLPDHVNDFTWYKNRKKSLGIKPVNKNIGLSIIIPTFNRSRILDITLACL 173
           Sequence 9, Application US/09283402;
GENERAL INFORMATION:
TOTAL OF PAUL DEANGELIS
TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA
TITLE OF INVENTION: MULTOCIDA AND USES THEREOF
TITLE OF INVENTION: MULTOCIDA AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/283,402
CURRENT FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VET. 2.0
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Best Local Similarity 89.9%; Pred. No. 0;
Matches 874; Conservative 28; Mismatches
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OTHER INFORMATION: either Asn, Asp, Glu
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INFORMATION: either Asn, Asp, Glu
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LOCATION: (164)
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                                                                                     Length 972;
                                                                                                              7;
                                                                                                              Indels
                                                                                     DB 16;
                                                                                                              63;
                                                either Asn, Asp, Glu or Gln
                                                                                    90.4%; Score 4601.5; 89.9%; Pred. No. 0;
                                                                                                             28; Mismatches
             either Ile or Val
                                                                                                 Best Local Similarity 89.9
Matches 874; Conservative
           OTHER INFORMATION:
                                               OTHER INFORMATION:
                       NAME/KEY: MOD_RES
LOCATION: (952)
LOCATION: (744)
                                                           US-09-283-402-9
                                                                                     Query Match
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                                                                                                                          Sequence 9, Application US/09469200

Sequence 9, Application US/09469200

GENERAL INFORMATION:

APPLICANT: Board of Regents of the University of Oklahoma

TITLE OF INVENTION: UNCLEIC ACID ENCODING HYALURONAN SYNTHASE AND METHODS

TITLE OF INVENTION: OF USE

FILE REPERENCE: 617022-7

CURRENT APPLICATION UNMER: US/09/469,200

CURRENT APPLICATION NUMBER: G/080,414

PRIOR APPLICATION NUMBER: 60/080,414

PRIOR FILING DATE: 1998-04-02

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 29

SOFURD NOS: 29

SOFURD NOS: 20
901 IDSVPEYNTEDIWEQFALLILEKKTGHVFNKTSTLTYMPWERKLQWTNEQIXSAKRGENI 960
                                                                                                                                                                                                                                                                                                                                                                                                                    Description of Artificial Sequence: consensus
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ORGANISM: Artificial Sequence
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                                PVNKFIINSITL 965
                                                   LOCATION: (253)
OTHER INFORMATION: e
NAME/KEY: MOD_RES
LOCATION: (479)
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LOCATION: (90)
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LOCATION: (192)
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LOCATION: (201)
OTHER INFORMATION: e
NAME/KEY: MOD_RES
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NAME/KEY: MOD_RES
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OTHER INFORMATION:
NAME/KEY: MOD_RES
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NAME/KEY: MOD_RES
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OTHER INFORMATION:
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LOCATION: (62)
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LOCATION: (952)
COTHER INFORMATION: either Asn, Asp, Glu or Gln
03-09-669-200-9
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                                                                                                                                                                                                                                                                                      either Asn, Asp, Glu or Gln
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Similarity 89.9%; Pred. No. 0;
                                               or
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                                               gIn
                                                                                              either Asn, Asp, Glu
                                                                         UNAMENTE: MOD_RES
LOCATION: (292)
OTHER INFORMATION: either Asn, Asp, Glu
NAMENCE: MOD_RES
LOCATION: (316)
OTHER INFORMATION: either Ile or Val
NAMENCE: MOD_RES
LOCATION: (329)
OTHER INFORMATION: either Phe or Tyr
NAMENCE: MOD_RES
LOCATION: (340)
OTHER INFORMATION: either Phe or Tyr
NAMENCE: MOD_RES
LOCATION: (405)
OTHER INFORMATION: either Phe or Tyr
NAMENCE: MOD_RES
LOCATION: (405)
OTHER INFORMATION: either Asn, Asp, Glu
NAMENCE: MOD_RES
LOCATION: (405)
OTHER INFORMATION: either Ile or Val
NAMENCE: MOD_RES
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                                                Asn, Asp,
INFORMATION: either Ile or
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Best Local Similarity 89.9%
Matches 874; Conservative
                                               either
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OTHER INFORMATION:
                                               OTHER INFORMATION:
NAME/KEY: MOD_RES
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                                                                                                                                                                                                                                             DNTLEVINKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELC
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                                                                                 EEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKEK
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GENERAL INFORMATION:
APPLICANT: Weigel, Paul
APPLICANT: DeAngelis, Paul
APPLICANT: Weigel, Paul
APPLICANT: RumarL, Kshama
TITLE OF INVENTION: Hyaluronan Synthase Gene and
FILE REFERENCE: 3554.011
CURRENT APPLICATION NUMBER: US/10/011,768B
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/064,435
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-36
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Version 3.1
FEMALE. PATENTING OF SECTION OF SE
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Sequence 56855, Application US/09791537

GENERAL INFORMATION:
APPLICANT: BHOOMLX Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT PILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0

SEQ ID NO 56855
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           7;
Length 972;
           60; Indels
DB 24;
     ; Pred. No. 0;
62; Mismatches
Score 4490.5;
      al Similarity 86.7
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                   Sequence 9, Application US/10011771B
GENERAL INFORMATION:
APPLICANT: Weigel. Paul H.
APPLICANT: Mengel.; Paul H.
APPLICANT: Kumari, Kshama
TITLE OF INVENTION: Hyaluronan Synthase Gene and
FILE REFERENCE: 3554.011
CURRENT APPLICATION NUMBER: US/10/011,771B
CURRENT FILING DATE: 2001-10-11
PRIOR FILING DATE: 1998-10-26
FRICH APPLICATION NUMBER: US 60/064,435
FRICH APPLICATION NUMBER: US 60/064,435
FRICH APPLICATION NUMBER: US 60/064,435
FRICH SEQ ID NOS: 10
SOFTWARE: PATCHING DATE: 1997-10-31
SOFTWARE: PATCHING VERSION 3.1
                                                                                                                                                                                                                                                                                                                                             88.2%; Score 4490.5; ilarity 86.7%; Pred. No. 0; Conservative 62; Mismatches
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Best Local Simi
Matches 843;
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US-10-011-771B-9
RESULT 15
US-10-011-771B-9
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121.219 Million cell updates/sec
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1 MNTLSQAIKAYNSNDYELAL......SAKKGENIPVNKFIINSITL 965
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Pending_Patents_AA_New:* Database :

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sednence	Sequence	Sequence	Sequence	Sednence	Sequence	Sequence	Sequence	
ID	US-09-842-484A-2	US-09-842-484A-4	US-10-217-613-3	US-10-217-613-8	US-10-217-613-9	US-09-469-200D-9	US-10-309-560-8	US-10-217-613-1	US-10-217-613-7	US-10-216-289-2	US-10-216-289-4	US-09-134-000C-5749	US-10-264-213-152	US-09-134-000C-5087	US-09-134-000C-6392	US-09-134-000C-5086	US-10-092-411A-4067	US-10-096-129-3	US-10-096-129-8	-960-0	US-10-303-161-39	0-303-1	US-10-303-118-39	US-10-303-128-39	US-10-303-134-39	US-10-303-161-27	
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% Query Match	100.0	9.66	99.6	9.66	90.5	88.2	88.2	61.0	61.0	44.3	44.3	9.9	5.9	5.5	4.9	4.7	4.5	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	_
Score	5089	2067	2067	2067	4604.5	4490.5	4486.5	3102.5	3102.5	2256.5	2256.5	333.5	599	262.5	248.5	240.5	227	210	210	209	208.5	208.5	208.5	208.5	208.5	207	
Result No.	-	7	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	

301 PSITSKGNISLDWRLEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNKVGWFDEEFNHWG 360

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361 GEDVEFGYRLFAKGCFFRVIDGGMAIHOEPPGKENETEREAGKSITLKIVKEKVPYIYRK 420

27 207 4.1 301 6 US- 28 207 4.1 301 6 US- 29 207 4.1 301 6 US- 30 207 4.1 301 6 US- 31 205 4.0 389 6 US- 32 205 4.0 389 6 US- 34 205 4.0 389 6 US- 35 205 4.0 389 6 US- 36 204 4.0 389 6 US- 37 200.5 3.9 303 6 US- 41 200.5 3.9 303 6 US- 42 200.5 3.9 303 6 US- 42 200.5 3.9 303 6 US- 43 199 3.9 297 6 US- 44 199 3.9 297 6 US- 45 199 3.9 297 6 US- 46 199 3.9 297 6 US- 47 199 3.9 297 6 US- 48 111 US DATE: 2000-04-25 45 US- 46 US- 47 199 3.9 297 6 US- 48 11 US DATE: 2000-04-25 48 US- 48 18

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Sequence 3, Application US/10217613
GENERAL INFORMATION:
APPLICANT: DEANGELLS, PAUL
TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA ANI
TITLE OF INVENTION: THERROF
FILE REFERENCE: 35541.081
CURRENT APPLICATION NUMBER: US/10/217,613
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/283,402
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GENERAL INFORMATION:
TITLE OF INVENTION NUMBER: 0.009842484A

FILE REFERENCE: 4605.003
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Version 3.1
SEQ ID NO 4.5
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960; Conservative 2; Mismatches
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ORGANISM: Pasteurella multocida
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Sequence 8, Application US/10217613
Sequence 8, Application US/10217613
GENERAL INFORMATION:
APPLICANT: DEANGELIS, PAUL
TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA AN
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 35541.081
CURRENT PAPLICATION NUMBER: 09/283,402
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VEYSION 3.1
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Pred. No. 0;
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/080,414
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 09/178,851
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VECSION 3.1
SEQ ID NO 3
                                                                                                                           TYPE: PRT ORGANISM: Pasteurella multocida
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99.58;
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Best Local Similarity 99.5'
Matches 960; Conservative
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OTHER INFORMATION: either Asn, Asp, Glu or Gln
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OTHER INFORMATION: either Asn, Asp, Glu or Gln
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OTHER INFORMATION: either Asn, Asp, Glu or Gln
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OTHER INFORMATION: either Asn, Asp, Glu
FEATURE:
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OTHER INFORMATION: either 11e or Val
FEATURE:
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LOCATION: (243)..(243)
OTHER INFORMATION: either Ile or Val
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OTHER INFORMATION: either Ile or Val
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OTHER INFORMATION: either Ile or Val
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OTHER INFORMATION: either Ile or Val
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OTHER INFORMATION: either Phe
                                      LOCATION: (113)..(113)
OTHER INFORMATION: either Ile
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OTHER INFORMATION: either
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OTHER INFORMATION: either
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APPLICANT: DEANGELIS, PAUL
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE REPERENCE: 35541.081
CURRENT APPLICATION NUMBER: US/10/217,613
CURRENT APPLICATION NUMBER: US/283,402
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-02
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-10-26
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LOCATION: (90)...(90)
OTHER INFORMATION: either Asn, Asp, Glu or Gln
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NAME/KRY: MISC_FEATURE
LOCATION: (17)..(17)
OTHER INFORMATION: either Asn, Asp,
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OTHER INFORMATION: either Asn, Asp,
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SOFWARE: Patentin version 3.1
SEQ ID NO 9
ERNCTH: 972
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US-10-217-613-9
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89.9%; Pred. No. 0;
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                                                       FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (952)..(952)
OTHER INFORMATION: either Asn,
US-10-217-613-9
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                                                                                                        Query Match
Best Local Similarity 89.9°
Matches 874; Conservative
NAME/KEY: MISC_FEATURE
LOCATION: (439)..(439)
OTHER INFORMATION: either
                       FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (744)..(744)
OTHER INFORMATION: either
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APPLICANT: DeAngells, Paul
APPLICANT: DeAngells, Paul
APPLICANT: Constant, Ksham
TITLE OF INVENTION: Hyaluronan Synthase Gene and
FILE REFERENCE: 3554.01
CURRENT PAPLICATION NUMBER: US/09/469,200D
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/064,435
PRIOR FILING DATE: 1998-10-26
PRIOR RILING DATE: 1998-10-36
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
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GENERAL INFORMATION:
APPLICANT: WEIGEL, PAUL H
APPLICANT: WEIGEL, PAUL H
TITLE OF INVENTION: HYALURONAN SYNTHASES AND METHODS OF MAKING AND USING SAME;
TITLE OF INVENTION: HYALURONAN SYNTHASES AND METHODS OF MAKING AND USING SAME;
FILE REFERENCE: 35541.082
CURRENT APPLICATION NUMBER: US/10/309,560
CURRENT PILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: 60/336,105
PRIOR APPLICATION NUMBER: 60/336,105
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PATENTIN VETSION 3.1
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                                                                                                                       MNTLSQAIKAYNSNDYELALKLFEKSAETYGRKIVEFQIIKCKEKL----STNS---YVS
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                                                                QSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYP
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                                                                                                                                                               DWIEKINAHPPFKKLIKTYFNDNDLRSMNVKGASQGMFMKYALPHELLTIIKEVITSCQS
LKEFLKDKTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHL
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86.6%; Pred. No. 0;
iive 63; Mismatches
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ORGANISM: Pasteurella
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US-10-309-560-8
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Sequence. 1, Application US/10217613
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Sequence. 1 Application US/10217613
GENERAL INFORMATION:
APPLICANT: DEANGELIS, PAUL
TITLE OF INVENTION: DNA ENCODING HYALURONAN SYNTHASE FROM PASTURELLA MULTOCIDA AND
TITLE OF INVENTION: THEREF
FILE REPERENCE: 35541.081
CURRENT APPLICATION NUMBER: US/10/217,613
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/283,402
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 9
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                                                 DFVSILDCDMAPQQLWVHSYLTELLEDNDIVLIGPRKYVDTHNITAEQFLNDPYLIESLP
                                                                                                                                  EEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKEK
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APPLICANT: SUGIURA, NOBUO
APPLICANT: KIMATA, KOJI
TITLE OF INVENTION: CHOUDROITIN POLYMERASE AND DNA ENCODING THE SAME
FILE REFERENCE: 226882USO
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                                                                                                                                        61.0%; Score 3102.5; DB (82.6%; Pred. No. 1.5e-287; ive 57; Mismatches 58
              09/178,851
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                                                                                                     Pasteurella multocida
                                                  version 3.1
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 09/1
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                   581; Conservative
                                                                                                                                                      Similarity
                                                                           703
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                                                                                                     ORGANISM:
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                                                                                                                                                                                                                                                                                              VNQKTNYPFEVVVADDGSKENLLTIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKY
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                                                                                     2.5; DB 6; Length 703;
1.5e-287;
                                                                                                                                        1 MNTLSQAIKAYNSNDYELALKLFEKSAETYGRKIVEFQIIKCKEKL----STNS-
                                                                                                                 Indels
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                                                                                       61.0%; Score 3102.5; 82.6%; Pred. No. 1.5e
                                                                                                               57; Mismatches
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TITLE OF INVENTION: DNA ENCODING HYALURONAN
TITLE OF INVENTION: THEREOF
FILE REPERENCE: 35541.081
CURRENT APPLICATION NUMBER: US/10/217,613
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/283,402
PRIOR APPLICATION NUMBER: 09/283,402
PRIOR APPLICATION NUMBER: 09/283,402
PRIOR APPLICATION NUMBER: 60/080,414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 7, Application US/10217613; GENERAL INFORMATION:
                                                   multocida
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                                                ORGANISM: Pasteurella
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  SOFTWARE: Patentin
           SEQ ID NO 1
LENGTH: 703
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                                      TYPE: PRT
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APPLICANT: NINOMIYA, TOSHIO
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                                                                                                                                                                DB 6;
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                                                                                                                                                               44.3%; Score 2256.5; DB (ilarity 61.3%; Pred. No. 9.8e-207; Conservative 112; Mismatches 148;
CURRENT APPLICATION NUMBER: US/10/216,289
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: UP 2001-244685
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: UP 2001-324127
PRIOR APPLICATION NUMBER: UP 2002-103136
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
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US-10-216-289-2
                                                                                                                                                                         Local Similarity
es 419; Conserv
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US-10-216-289-4
                                                                                                      SEQ ID NO 2
LENGTH: 686
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                                                                                                                          TYPE: PRT
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Matches
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Sequence 4, Application US/10216289 GENERAL INFORMATION:

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RKLLPIEDSHIHRIPLVSIYIPAYNCANYIQRCVDSALNOTVVDLEVCICNDGSTDNTLE 478
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APPLICANT: KIMATA, KOJI
TITLE OF INVENTION: CHONROTIIN POLYMERASE AND DNA ENCODING THE SAME
FILE REFERENCE: 226882USO
CURRENT APPLICATION NUMBER: US/10/216,289
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: UP 2001-244685
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-2
PRIOR FILING DATE: 2001-02-2
PRIOR FILING DATE: 2001-02-2
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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Matches 419; Conserv
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242 VYPDLQIASQRRVLYAYISTLNQMQNVDGYQEIREQLISKIKELRK--PVLEDHKAPIRD 299
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                                             --ASGVIDFVYMGDNTKII---- 716
                                                                                              HDSLFVKNDSYAYMKKYDVGMNFSALTHDWIEKINAHPPFKKLIKTYFNDNDLRSMNVKG 865
                                                                                                                                              .----EKG 745
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755 AFYHKHQVN------ILLNNDISYYTSNRLIKTEAHLSNINKLSQLNLNCEYIIFDN 805
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; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TTPLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Havukkala, Ilkka J
APPLICANT: Havukkala, Ilkka J
APPLICANT: Labbers, Mark William
APPLICANT: Lokker, James
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them, and methods for using them.
FILE REFERENCE: 11000.1043.c3
CURRENT APPLICATION NUMBER: US/10/264,213
CURRENT FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 152
LENGTH: 331
                                                                                                                                                                                                                                                                                          915 EKKTGHVFNKTSTLTYMPWERKLQWTNEQIQSAKKGENIPVNKFIINSIT 964
                                                                                                                                                                                                                                                                                                                         Length 331;
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ilarity 27.9%; Pred. No. 2.7e-20;
Conservative 58; Mismatches 131; Indels
                                                                                                                               673 FGQEKTQGNGTAIEMFSIIIADND----TSN-
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US-10-264-213-152
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Best Local Similarity
Matches 87; Conserve
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US-09-134-000C-5087
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                                                             Sequence 5749, Application US/09134000C
GRERAL INFORMATION:
APPLICAMY: Lynn Doucette-Stamm et al
ITILE OF INVENTION: BUTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 5149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  546 VYTTNRNVNPDGSLIANG--YNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIEN 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----NR------QGINYYNYDKFD--DLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIAVSIFYPNTLNGL--VKKLNNIIEYNKNIFVII---LHVDKNHLTPDIK----KEIL 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::| : | | : | | ::
ENVTWDEEIKSYGDTGLFWKINSASQNVIFIKDCLYFYRQDNPNSTVNNVATKVPFLFQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 504 FVGEDAYFTYTALLGTEKIVALNKYLLTRIVRQDGL-MSTYGMNYRDEFNLHDKMLEYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  604 AVDYDMFL---KLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVVNQSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.6%; Score 333.5; DB 5; 20.8%; Pred. No. 7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 198; Conservative 156; Mismatches 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-134-000C-5749
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CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION UNBER: US 60/055,778
PRIOR APPLICATION UNBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                  22;
 ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    530 VELCLKEFLKDKTLACVYTINRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIR 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 ILEEIGGFRKGYEGSQDYDLVLRFTEKTTKERIKHIPKVLYYRRMLPTSTAVDQGSKGYA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKNHFVVVNQSLNRQGINYYN-----YDKFDDLDESRKYIFNKTAEYQEEMDMLKDL 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LVSIIIP-TKNGYKDVQRCVSSIIEKTTYQNYEIIMADNGSTDPKMHELY 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413 KVPYIYRKLLPIEDSHIHRIPLVSIYIPAYNC-ANYIQRCVDSALNQTVVDLEVCICNDG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| | : : | : : | | : | | : | | EVLDI -- EAMTQEIATFHYQPKISIAMPVNNVEEKWLRLCIDSILNQVYTNWELCMADDA 232
                                                                                                                                                                                                                                                                                                                                                                                                                       73 NQIYQTEPAIEAGFVVTLEGIKQKKVL----PFHFQSSAHVITVDFPLNKKYPVIPGTE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKE 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------LEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNK-----VGWF 352
                                                                                                                                                                                                                                                                                                                   260 DNDIVLEGPRKXVD--THNITAEGFLNDPYLIESLPETAINNNPSITSKGNISLDWR--- 314
                                                                                                                                                                                                                                                                                                                                              590 AWHLTDGFNENIENAVDYDMFLKLSE---VGKFKHLNKICYNRVLHGDNTSIKK--LGIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STD-NTLEVINKLYGNNPRVRIM-SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                697 KLIQNKDAKIAVSIFYPNTLNG---LVKKLNNIIEYNKNIFVIILHVDKNHLTP-----
                                                                                                                                                                                                                                                                                    Indels 111;
                                                                                                                                                                                                                                                 Length 534;
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                                                                                                                                                                                                                                               5.2%; Score 262.5; DB 5;
larity 23.0%; Pred. No. 1.9e-16;
Conservative 100; Mismatches 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DIKKEILAFYHKHQVNILLNNDISYYTSNRLIKTEAH 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEFEQQLPGRFFVESIDIPFN----FSTINNRAAKKAH 534
TITLE OF INVENTION: ENTERCOLL.
FILE REFERENCE: 0327956-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 5087
LENGTH: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
S.09-134-000C-6392
Sequence 6392, Application US/09134000C
GENERAL INFORMATION:
                                                                                                                                                                                 erococcus faecalis
87
                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Ent
US-09-134-000C-50
                                                                                                                                                                                                                                                                     Best Local Sim
Matches 133;
                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                           663 YYNYDKFDDLDESRKY1FNKTAEYQEEMDMLKDLKLIQNKDAKIAVS----IFYPNTL-- 716
                                                                                                                                                                                                                                                                                                                                                                                                                                 432 IPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVR 491
                                                                                                                    Gaps
                                                                                                                                                                      492 IMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLK---DKTLACVYT
                                                                                                                                                                                                                                                                                                                                               509 MFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGIN-----
                                                                                        Length 330;
                                                                                                                                                                                                                                                                                                     -----NGLVKK-LNNIIEYNKNIFVIILHVDKNHLTPDIKK 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: January 4, 2003, 02:45:48 Job time : 565 secs
                            TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                          Query Match 4.9%
Best Local Similarity 24.9%
Matches 85; Conservative
                                                          US-09-134-000C-6392
SEQ ID NO 6392
             LENGIH:
                                                                                                                                                                                                                                                       29
                                                                                                                                                                                                                                                                                                                                                                                    163
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

January 4, 2003, 02:18:59 ; Search time 69 Seconds (without alignments) 1344.489 Million cell updates/sec Run on:

US-09-842-484A-2 5089 1 MNTLSQAIKAYNSNDYELAĻ......SAKKGENIPVNKFIINSITL 965 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	glucuronosyltransf	hypothetical prote	ທ	hypothetical prote	hypothetical prote	glycosyltransferas	glycosyltransferas	hypothetical prote	hypothetical prote	_	hypothetical prote	glycosyl transfera	beta-1,3-N-acetylg	hypothetical prote	teichuronic acid b	capsular polysacch	minor teichoic aci	hypothetical prote	glycosyltransferas	glycosyl transfera	hypothetical prote	glycosyltransferas	lacto-N-neotetraos	probable sugar tra			qlycosyl transfera	qlycosyl transfera	probable regulator
SUMMARIES	ID	T09595	E97757	AB1211	D95206	AD2189	A84114	B97168	AG2188	AB2190	B75096	AH2026	T44330	T50038	AE2189	E84107	A70037	E71690	AH2189	A97168	T44647	AE1876	н97167	D81027	F81289	E81318	H69814	S70813	H64130	E91190
	BB :	7	7	7	~	7	7	7	~	7	7	7	7	~	7	7	7	-	7	7	7	~	7	7	7	~	7	Н	Н	~
	Length	972	604	327	969	323	303	333	321	324	298	333	340	306	316	257	344	318	318	336	322	1013	333	349	116	389	392	333	7	338
d	Query Match	88.2	5.8	5.7	5.3		5.1	5.1	5.0	5.0	4.9	4.7	4.7	4.7	4.7	4.7	4.7	4.6	4.6	4.6	4.6	4.6	4.6	4.5	4.5	4.5	4.5	4.5	4.4	4.4
	Score	4486.5	294	292.5	268.5	264.5	261.5	258.5	256	254.5	251	241	239	238	238	237.5	237	235.5	235	234.5	234	233.5	232	229.5	229.5	229	228	227.5	224.5	223.5
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probable regulator	hypothetical prote	hypothetical prote	glycosyltransferas	probable sugar tra	probable glycosyl	hypothetical prote	hypothetical 40.5K	probable glycosylt	probable galactosy	lacto-N-neotetraos	glycosyl transfera	probable two-domai	glycosyl transfera	hypothetical prote
F86037	AH2188	G71153	E97083	B81289	AG0023	AG2189	ОЗЕСТН	G95948	C81318	н81970	F95205	B81318	A64099	AI2404
010	۰ ۵	-	~	7	7	~	-	7	~	~	7	~	~	~
338	330	334	338	445	329	318	344	367	390	346	301	515	250	313
4.4	. 4	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.2	4.2	4.2	4.2	4.2	4.2
223.5	221	221	221	220.5	220	218.5	217.5	217	216	215.5	214.5	214.5	214	214
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT	1
T09595 glucuro N;Alter	19295) glucuronosyltransferase (EC 2.4.1.17) - Pasteurella multocida N/Alternate names: hyaluronan synthase
C;Speci C;Date:	tes: Pasteurella multocida : 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 : mostos
R; DeAng	satun: 105757 gelis, P.L., Jing, W.; Drake, R.R.; Achyuthan, A.M. - Chom 773 A464-8458 1998
A;Title A;Refer	A:Title: Identification and molecular cloning of a unique hyaluronan synthase from A;Reference number: 216757; MUID:98192645; PMID:9525958
A; Acces A; Statu	ssion: T09595 us: preliminary; translated from GB/EMBL/DDBJ
A; MOLEC A; Resid	cule type: DNA lues: 1-972 <dea></dea>
A; Cross A; Exper	A;Cross-references: EMBL:AF036004; NID:93043922; PIDN:AAC38318.1; PID:93043923 A;Experimental source: strain P-1059; ATCC 15742
C;Genetics: A;Gene: HAS	ics: : HAS
C;Function: A;Descripti C;Keywords:	C.Function: A.Description: polymerizes hyaluronan (HA, hyaluronate, hyaluronic acid) polysacchar C.Keywords: capsule synthesis; glycosyltransferase; hexosyltransferase; hyaluronic a
Quer)	Ouery Match 88.2%; Score 4486.5; DB 2; Length 972; Best Local Similarity 86.6%; Pred. No. 1.28-238;
Match	Matches 842; Conservative 63; Mismatches 60; Indels 7; Gaps 2;
ΟŊ	1 MNTLSQAIKAYNSNDYELALKLFEKSAETYGRKIVEFQIIKCKEKLSTNSYVS 53
QΩ	1 MNTLSOAIKAYNSNDYQLALKLFEKSAEIYGRKIVEFQITKCQEKLSAHPSVNSAHLSVN 60
Qy	54 EDKKNSVCDSSLDIATQLLLSNVKKLTLSESEKNSLKNKWKSITGKKSENAEIRKVELVP 113
qa	61 KEEKVNVCDSPLDIATQLLISNVKKLVLSDSEKNTLKNKWKLLTEKKSENAEVRAVALVP 120
0y 1	114 KDFPKDLVLAPLAPLPDHVNDFTWYKNRKKSLGIKPVNKNIGLSIIIPTFNRSRILDITLACL 173
Db 1	121 KDFPKDLVLAPLPDHVNDFTWYKKRKRLGIKPEHQHVGLSIIVTTFNRPAILSITLACL 180
0y 1	174 VNQKTNYPFEVVVADDGSKENLLIIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKY 233
Db 1	181 VNQKTHYPFEVIVTDDGSQEDLSPIIRQYENKLDIRYVRQKDNGFQASAARNMGLRLAKY 240
, vo	234 DFVSILDCDMAPQQLWVHSYLTELLEDNDIVLIGPRKYVDTHNITAEQFLNDPYLIESLP 293
qu	241 DFIGLLDCDMAPNPLWVHSYVAELLEDDDLTIIGPRKYIDTQHIDPKDFLNNASLLESLP 300
, yo	294 ETATNNNPSITSKGNISLDWRLEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNKVGWFD 353
qa	301 EVKTNNSVAAKGEGTVSLDWRLEQFEKTENLRLSDSPERFFAAGNVAFAKKWLNKSGFFD 360
Qy	354 EEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKEK 413

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glycosyltransferases homolog lmol090 [imported] - Listeria monocytogenes (strain EGD glycosyltransferases homolog lmol090 [imported] - Listeria monocytogenes (c; becies: Listeria monocytogenes (c; bate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 Rights All 2012 Paranal, G.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloek, D.; Jones, L.M.; Karst, U. Science 24, 849-852, 2001 A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Allitle: Comparative genomics of Listeria species. A.; Title: Comparative genomics of Listeria species. A; Reference number: AB1077; MUID:21537279; PMID:11679669 A; Accession: AB121 Asian Asian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSPDB:GN00177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRI 492
                                                                                                                                                                                                                                                                                                                                                                                                           385
                                                                                                                                                                                                                                                                            LIQNKDAKIAVSIFYPNTLNGLVKKLNNI-IEYNKNIFVIILH----VDKNHLTPDIKKE 752
                                                                                                                                                                                                                                                                                                                                                                    811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426
                                     MSKPNGGIASASNAAVSFAKGYYIGQIDSDDYLEPDAVELCLKEFLKDKTLACVYTTNRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNPDGS-----LIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGF---
                                                                                                                                 ECNVIWSSFIHELTEBEMIKMEGSPYL-----FLTRTATFLSNNT-PYKKACDLANTWA
                                                                                                                                                                                                                                                                                                        :: |:|
------KGKYIESVHSGLF
                                                                                                                                                                                                                                                                                                                                                                    -ILAFYHKHQVNILLINNDISYYTSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFV
                                                                                                                                                                                                                                                                                                                                                                                           812 KNDSYAYMKKYDVGMNFSALTHDWIEKINAHPPFFKKLIKTYFNDNDLRSMNVKGASQGMF
                                                                                                                                                                                           647 N------HFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLK
                                                                                                   TIRAWHLTDGFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKK
           -TINRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMF
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A; Residues: 1-527 <GLA>
A; Cross-references: GB:NC_003210; PIDN:CAC99168.1; PID:g16410492;
A; Cross-references: strain EGD-e
C; Genetics:
A; Gene: Imo1090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-DKIEIQLKFMEENNF-IFSHTSYHKINE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGNVFP-----40VIQTC 438
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                    LKEFLKDKTLACVY -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein RC0461 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Date: 30.Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C;Accession: E97757
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2039-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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DNTLEVINKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELC
                                                                   VPYIYRKLLPIEDSHIHRIPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 604;
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llarity 24.8%; Pred. No. 1.1e-08;
Conservative 71; Mismatches 213; Indels
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Matches 124; Conserv
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-604 <KUR>
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hypothetical protein alr3067 (imported] - Nostoc sp. (strain PCC 7120)
C.Species: Nostoc sp.
A.Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C.Racession: AD2189
R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irit, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabat DNA Res. 8, 205-213, 2001
A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A.Reference number: AB1807; MUID:21595285; PMID:11759840
A.Recession: AD2189
A.Status: preliminary
A.Residues: 1-323 <KUR>
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Clypecies: Bacillus halodurans
Clypecies: Dac-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
Clyacession: A84114
Rlyakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Actus: preliminary
A;Molecule type: DNA
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A, Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07432.1; GSPDB
A, Experimental source: strain C-125
C;Genetics:
A;Gene: BH3713
                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:BA000019; PIDN:BAB74766.1; PID:g17132161; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 YYKFANEADSYADESNSFAGDVYAELLIKNFLQNGSN-PLIRRAAIDSVGL------ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----FDPTLKSCEDWDFYLRLAAKWQFALVKKAQIIYRQ---SPTAMTSKLDVMEK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSIVIERAFNAAPPQLQHLKK-----QSLAWVYRFTAQQCLKYNSHKLADIKLAA-KRL 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.2%; Score 264.5; DB 2;
25.4%; Pred. No. 2e-07;
tive 64; Mismatches 116;
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26.5%; Pred. No. 2.7e-07;
tive 60; Mismatches 95
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                                                                                                                                                                                                                                                          hypothetical protein SP1771 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: O3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: D95206
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: D95206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE005672; PIDN:AAK75845.1; PID:914973268; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLK---EFLKDKTLACVYTTNR 551
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648 HFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDL---KLIQNKDA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 ALVDAMSERITLLANMGYPLEKHLAVYRQMLEVSLAN----GQASGLSDTATY----KE
                                                                                               705 KIAVSIFYPNTLNGLVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKH 760
                                                                                                                              Length 696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           594 -----TDGFNENIENAVDYDMFLKLSEVGKFKHLNKICY-NRVLHGD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match | 5.3%; Score 268.5; DB 2; Best Local Similarity 20.5%; Pred. No. 3.5e-07; Matches 101; Conservative 96; Mismatches 181;
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LIDVTNEWHDKVD 471
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A Molecule type: DNA
A; Residues: 1-696 <KUR>
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Cippedies: Nostoc sp.
A, Note: Nostoc sp.
A, Note: Nostoc sp. strain pcc 7120 is a synonym of Anabaena sp. strain pcc 7120
C, Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C, Accession: AG2188
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A; Ritle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Accession: AG2188
A; Accession: AG2188
A; Accession: AG2189
A; Molecule type: DNA
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hypothetical protein alr3073 [imported] - Nostoc sp. (strain PCC 7120)
6. Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
6. Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
6. Accession: ABA2190
8. Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigus Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabatai DNA Res 8, 2055-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MUID:2159285; PMID:11759840
A;Accession: AB2190
A;Accession: AB2190
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <RURS
A;Residues: 1-324 ×RURS

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                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-311 <KUR>
A; Residues: 1-321 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB74761.1; PID:g17132156; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        605 V-DYDMFLKLSEVGKFKHLNK-ICYNRVLHGDNTSIK------KLGIQKKNHFVVVNQS 655
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26.2%; Pred. No. 7.1e-07;
Live 63; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118;
                                                        sb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.0%; Score 256; DB 2;
ilarity 27.5%; Pred. No. 5.8e-07;
Conservative 50; Mismatches 118
                                                  hypothetical protein alr3062 [imported] - Nostoc
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nes 78; Conserv
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Matches 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycosyltransferase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: B97168
R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Daly, M.J; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J; Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97168
A;Status: preliminary
A;Molecule type: DM>
A;Residues: 1-333 < kUR>
A;Cross-references: GB.AB001437; PIDN:AAK80133.1; PID:g15025169; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 LVSIYIPPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIM 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  494 SKPNG-GIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDK---TLACVYTT 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        550 NRNVNPDGSL-IANGYNWPEFSREK-----LTTAMIAHHFRMFTIRAWHLTDGFNENIEN 603
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                                                                                                                                                                                                            549 ---TWRNVNPDGSLIANGYNWPE----FSREKL-----TTAMIAHHFRWFTIRAWHLTD 595
                                                                                                                                                                                                                                                    --GFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN 653
                                                                                                                                                                                                                                                                                                                                                                                        167 CGMFDEKLKARQDYDLWI------RVC-----RVC-----QKTLVGVVN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSLNRQGINYYNYDKFDDL-DESRKY------IFNKTAE----YQEEMDMLK 694
                                                                                                                                                62 YHPAKGGNYARNTGIKNAKGEFIAFLDDDDEWMPDKLELQIKEFNQNANVGLVYTGVEII 121
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::|::|||| |::|| |::|| |:|| |::::||| :::||| :::||| :::||| |:::||| MISVIMPVYNCEKYLHESIESILKQTYRDFEFIIVNDGSNDKSIDIINKYANDDNRIVVV
                                                                                           195 -KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ::|: |:| | | | | | :: :: ::| VNKALRNQSPKVARAYLKNSFLKRPTLTAIIMYMLSFLKY 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.1%; Score 258.5; DB 2; 26.4%; Pred. No. 4.4e-07; tive 54; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TEDYNLWLRAIAKGYKIAMLEEKLMKIRLHNDS----
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Best Local Similarity
Matches 81; Conserv
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QQ	1 MPKISVIIPAYNAERTILETINSVLNQTFSDLEIIVINDGSTDRTVEVLQNVDDARLK 58	Db 264 SIAIAPLNLENYMILLKLALDSRTVEYIKRILS 296
oy do	492 IMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNR 551 :	RESULT 11 AH2026
οy	552 NVNPDGSLIANGYNWPEFSREKLFTAMIAHHFRWFTIRAWHLTDGFNENIENAVDYDMFL 611	hypothetical protein all1766 [imported] - Nostoc sp. (strain PCC 7120) C.Specias: Nostoc sp. A.Note: Nostoc sp. strain PCC 7120 is a suppnum of Anabaena sp. strain PCC 7120
qq	Id	C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C; Accession: AH2026
oy a	612 KLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINYY 664 1. :	R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irig Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabat DNA Res. R. 205-213, 2001
à à	NYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKL-IQNKDAKIAVSIFYPNTLNGLVK-K	A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AH2026
g ć	ZUORRSVTSKSFKLQIIREASLAILDKAMKVLPLELQYLKKHS 239 723 LNNIIEYNKNIFVIILHVDKNHLTPDIK	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-33 <kur> A;Coss-references: GB:BA000019: PIDN:BAB73465.1: PID:a17130856: GSPDB:GN00179</kur>
අ දු	240 LSNIYRYNVELYLDSINNNSTVDIKYVIGNLLSYIRSRPQTLKEIYTYKLIIKIL 294 766 LNNDISYYTSNRLIKTEAHLSNI 788	A; Experimental source: strain PCC 7120 C; Genetics: A; Gene: all1766
g	295 LVIVLSPKLMSRLLQFIKKSKQMKNL 320	Query Match 4.7%; Score 241; DB 2; Length 333; Best Local Similarity 26.4%; Pred. No. 4.1e-06; Matches 70: Conservative 53: Mismatches 94: Indels 48: Gaps 7:
RESULT B75096	RESULT 10 875096	TPLVSTYIPAXNCANYORCVDSALNOTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVR 491
91yc C; Sp	- Pyrococcus abyssi (strain Orsay)	
C; Da	C:Date: JU-Mang-1999 #sequence_revision JU-Aug-1999 #text_cnange ZU-Jun-2000 C:Accession: B75096 R:Anonymous, Genoscope	492
Subr. A; De	Supmitted fo the EMBL Data Library, July 1999 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru A;Reference number: A75001	DD 66 IFSFENAGGNVSRNRGLALAVGREISFLDADDIWTPNRLESQLEALHNNPGFHVAXSWID 125 Ov 552 NVNPDGSLJANG
A; Ac	A;Accession: B75096 A;Status: preliminary	: : : 126 YIDEDGNFLISGRRVTLNGDVYKK
A; Re A; Cr A; Cr	A;Molecule 1798: DNA A;Residues: 1-98 cKAW> A;Cross references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50071.1; PID:g545856 A;Experimental source: strain Orsay	QY 595 DGFNENIENAVDYDMELKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVV 652
A; Ge C; Su	C.Jenetics: A.Gene: PAB0772 C.Superfamily: Neisseria meningitidis glycosyl transferase A	653NQSLNRQGINYNY
Ou Be Ma	Query Match 4.9%; Score 251; DB 2; Length 298; Best Local Similarity 24.3%; Pred. No. 9.8e-07; Matches 81; Conservative 66; Mismatches 136; Indels 50; Gaps 8;	DD 250 ENAYQAKFALGNHILHLSIANLINI 234 RESULT 12
oy Db	GGTDNTLEVINKLYGNNPRVR- 491 : : : ASTDNTPEVVESIEDGRIRY 61	T44330 glycosyl transferase homolog [imported] - Vibrio cholerae C;Species: Vibrio cholerae C;bate: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
ô	550	C;Accession: T44330 R:Vzmasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Gane 377 371-337 1999
С	IRLKKNSGGPIARNIGIKKAKGRFIALLDDDDEWLPHRLEVOVRKFENLGKEFGVVYGGF 121	Aritie: The genes responsible for O-antigen synthesis of Vibrio cholerae 0139 are c A:Reference number: 222749; MUID:99453293; PMID:10521656
oy B	551 RNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIENAV 605	A; Accession: T44330 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
oy G	606 DYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINYYN 665	A.Residues: 1-340 <ram> A.Residues: 1-340 <ram> A.Cross-references: EMBL:AB012957; NID:94115688; PIDN:BAA33634.1; PID:93721684 A.Experimental source: strain 022 C.Genetics:</ram></ram>
ò	NKDAKIAVSIFYPNTLNGLVKKLN- 724	A;Note: wblc C;Superfamily: Neisseria meningitidis glycosyl transferase A
9 6 7	RLIRKHLDIWKNPK OKNHLTPDIKKEII	Query Match 4.7%; Score 239; DB 2; Length 340; Best Local Similarity 25.4%; Pred. No. 5.4e-06; Matches 78; Conservative 56; Mismatches 113; Indels 60; Gaps 11;
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Gispedies: Nostoc sp.
A;Note: No
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A;Molecule type: DNA
A;Residues: 1-257 <STO>
A;Coss-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07380.1; GSPDB: A;Experimental source: strain C-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:BA000019; PIDN:BAB74767.1; PID:g17132162; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               552 NVNPDGSLIANGYNWPEFSREK------LTTAMIAHHF-:----RMFTIRA 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|: : |:| | |: : :|
105 QQHPEAGV---AYSWTYFMDEQGKSSIPGVSLFFEGDVQAHLLVNNFLASGSNPLIRKQA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VV--NQSLNRQGINYYNYDKFDDLDESRKYIFNKTAE-YQEEMDMLKDLKLIQNKDAKIA 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 VVRKHQIFYRQSATSMSSTKVKNMEDDGLFVVEKTFQSVKPELQYLKNQSL----- 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432 IPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVR 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        591 WHLTDGFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFV
                                                                                                                                                                                            hypothetical protein alr3068 [imported] - Nostoc sp. (strain PCC 7120)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.7%; Score 238; DB 2; Length 316
Best Local Similarity 24.5%; Pred. No. 5.5e-06;
Matches 78; Conservative 50; Mismatches 109; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             708 VSIFYPNTLNGLVKKLNNI 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 AWIYQYSTQQYLKQNVNNI 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-316 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: alr3068
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A; Reference number: Z25028; MUID: 98043549; PMID: 9383201 A; Reference number: Z25028; MUID: 98043549; PMID: 9383201 A; Reference number: Z25028; MUID: 98043549; PMID: 9383201 A; Residues: DNA A; Residues: 1-306 CKOLD.
A; Cross-references: EMBL: X85787; PIDN: CAAS9781.1 A; Experimental source: isolate NCTC 11902; serotype 14 A; Experimental source: isolate NCTC 11902; serotype 14 A; Experimental source: isolate NCTC 11902; serotype 14 A; Experimental source: isolate holyozichion: necessary for the addition of the third sugar in the synthesis of the type A; Pathway: capsular polysaccharide biosynthesis
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                                                                                                                                                                                                                                                                                                                               | : | || :: | || :: | || 231 QVQTKQLEKLGLKLNDEEMIMHFRLGLNAEMLFLNARADDV----KYYFNSILNANKKTQ 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDK----TLACVY---- 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    548 TT--NRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHF------RMFTIRAWHLTD 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENENIENAVDYDMFLKLSEVGKFKHLNK--ICYNRVLHGDNTSIKKLGIQKKNHFVVVN 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         654 Q-----SLN-----RQGIN---YYNYDKFDDLDESRKYIFNKTAEYQEEMD 691
                                                                                                                                                 493 MSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNRN 552
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                                               6 PISVIMSVYNGEKYLAQAIESILNQTFSDFEFIIVDDGSTDSSLSIIQAYMDKDDRIVL 65
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Search completed: January 4, 2003, 02:28:02 Job time: 75 secs

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OM protein - protein search, using sw model

January 4, 2003, 00:40:24; Search time 66 Seconds (without alignments) 606.434 Million cell updates/sec Run on:

US-09-842-484A-2 5089 1 MNTLSQAIKAYNSNDYELAL......SAKKGENIPVNKFIINSITL 965 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P55465 rhizobium s	Q57287 haemophilus	P11290 escherichia	-	P46918 bacillus su	P22639 anabaena sp	myxococcu	_		P57529 buchnera ap	_							P30195 staphylococ		P26401 salmonella	7	a	Q00383 epifagus vi		_		P52340 human herpe	<u>_</u>	P47534 mycoplasma	Q00402 saccharomyc	^	8295 methanoco	P39621 bacillus su
SUMMARIES	ID	Y4GI_RHISN	YF78_HAEIN	YIBD_ECOLI	Y868_HAEIN	GGAB_BACSU	YS86_ANASP	RFBC_MYXXA	Y025_MYCPN	GGAA_BACSU	EX5B_BUCAI	EX5B_BORBU	Y087_BUCAI	Y025_MYCGE	DPO3_UREPA	BXEN_CLOBU	TOXA_CLODI	RPC1_PLAFA	EPIB_STAEP	WCAA_ECOLI	RFBV_SALTY	EXOO_RHIME	BXEN_CLOBO	YCF1_EPIVI	KIP1_YEAST	Y060_MYCGE	TEGU_HSV6G	TEGU_HSV6U	RASO_METJA	Σ	NUM1_YEAST	RPM2_YEAST	DPOL_METJA	SPSA_BACSU
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7 methanococc	5 marchantia	8 plasmodium	2 mycoplasma	4 amsacta moo	6 mycoplasma	4 fowlpox vir	9 podospora a	4 haemophilus	4 schizosacch	2 methanococc	4 saccharomyc
058457	P0997	0000	P7504	P2981	P4760	09158	00152	04821	P4100	05824	90896
YA57_METJA	YCF2_MARPO	RBP1_PLAVB	Y060_MYCPN	NTP1_AMEPV	Y366_MYCGE	MCEL_FOWPV	DPOM_PODAN	YG96_HAEIN	CUT3_SCHPO	Y832_METJA	MYS1_YEAST
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154	154	153.5	153	152.5	152.5	152	150	149.5	149.5	148.5	148.5
34	35	36	37	38	33	40	41	42	43	44	4 5

ALIGNMENTS	31_	Y4GI. Rhizobium sp. (st Plasmid sym pNGRZ Plasmid sym pNGRZ Bacteria; Proteob Rhizobiaceae; Rhi NCBI_TaxID=394; [1] SEOUENCE FROM N. A MEDLINE-9730595; Freblerq C.A., Fe	Perret X.; "Molecular basis of symbiosis between Rhizobium and legumes."; Nature 387:394-401(1997) -!- SIMILARITY: STRONG TO M.XANTHUS O-ANTIGEN BIOSYNTHESIS PROTE RFBC (NOT TO BE CONFUSED WITH ENTEROBACTERIAL RFBC). This SWISS-PROT entry is copyright. It is produced through a coll between the Swiss Institute of Bioinformatics and the EMBL ou the European Bioinformatics Institute. There are no restrictio use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch) or send an email to license@isb-sib.ch).	EMBL HSSP Inte Pfam Hypo SEQU Suery M Best Lo	OY 20 LKLFEKSAETYGRKIVEFOIIKCKEKLSTNSYVSEDKKNSVCDSSLDIATOLLLSNVKKL 79 :: : :
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation ^{\circ}
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                                                                                                                  296 ATNNNPSITSKGNISLDWRLEHFKKTDNLRLCDSPFRY---FVAGNVAFSKEWLNKVGWF 352
                                                                                                                                                                                      ---GGMAIHQEPPGKEN 395
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                                                                                                                                                                                                                         533 REGFE--GAQDYDMLLR-----CIERVQDRQIHHIAKVLYSWRATPGSAAASNRAKPYAN
                                                                                                                                                                                                                                                         ETEREA------GKSITLKIVKEKVPYIYRKLLPIEDSHIHRIPLVSIYIPAYNCAN
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SYANWELCLADDCSTDPEVGRVLRNYAAQDPRVRVVFREANGH-MSQASNSAIEIARGAY
                                                 236 VSILDCDMAPQQLWVHSYLTELLEDNDIVLIGPRKYVDTHNITAEQFLNDPYLIESLPET
                                                                     Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
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-!- SIMILAGITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YE78_HAEIN STANDARD; PRT; 323 AA. 057287; 005077; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Putative 91ycosyl transferase H11578 (EC 2.-.-).
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=KIZ. / MG1655;
STRAIN=KIZ. / MG1655;
SOFIA H.J., Burland V., Daniels D.L., Plunkett G. III, Blattne Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattne "Analysis of the Escherichia coli genome. V. DNA sequence of "region from 76.0 to 81.5 minutess.";
Nucleic Acids Res. 22:2576-2586(1994).
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J. Biol. Chem. 264:5226-5232(1989).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYPYAEDYKFWSEVSRLGCLANYPEALVKYRLHGNQTS-------
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Aronson B.D., Somerville R.L., Epperly B.R., Dekker E.E.
"The primary structure of Escherichia coli L-threonine
                                                                                                                                                     Interpretion 173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                           323 AA; 37680 MW; 7CBC2681039AB5B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YIBD_ECOLI STANDARD; PRT; 344 AA. p11290; p22999; Created) 01-001-1989 (Rel. 11, Created) 01-007-1994 (Rel. 30, Last sequence update) 16-007-2001 (Rel. 40, Last annotation update) putative qlycosyl transferase yibD (EC 2...-).
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23.2%; Pred. No. 1.5e-05;
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Freymond P., Karamata D.;
                                                             Venter J.C.;
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P46918;
                                                                                                                                                                                                                                                                                                                                                 Query Match
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          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                     MMNSTNKLSVIIPLYNAGDDFRTCME -> MRAMISALVWK
                                                                                                                                                                                                                                                                                                                                                                                                                 121 -NADWCFRETGETWQSIPTDRLRSTGVLTGPDWLRMGLSSRRWTHVVWMGVYRRDVIVKN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   648 HFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQ------EEMDMLKDLKL 698
                                                                                                                                                                                                                                                                                                                                                435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
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MEDLINE-95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                |:: : : | : | | | | | | | ::
238 HYIKITRLLEKLNRNY--ADKIMIYPE----FHQQITYEALRVCHAVRKEPDILTRQRM
                                                                                                                                                                                                                                                                                                                                                                                                  495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKD--KTLACVYTTNRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 553 VNPDGSLIANGYNWPEFSREKLTTA------MIAHHFRMFTIRAWHLTDGFNENIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  604 AVDYDMFLKLSEVG-----GIQKKN
                                                                                                                                                                                                                                                                                                                          65;
                                                                                                                                                                                                                                                                                                  Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                      EcoGene; EG11266; yibb.
Interpro; IPR001173; G1ycos_transf_2.
Pfam: PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                           -> G (IN REF. 2).
9B5DABFE86D5457A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase H10868 (EC 2.-.-).
                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                         57; Mismatches 128;
                                                                                                                                                                                                                                                                                                4.3%; Score 217.5; DB 23.1%; Pred. No. 4e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   699 IQNKDAKIAVSIFYPNTLNGLVKKL 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 I----AEIFTS-----GMYKRL 303
                                                                                                        EMBL; U00039; AAB18592.1; -.
EMBL; AE000439; AAC76639.1; -.
EMBL; X06690; CAA29885.1; -.
PIR; A30268; Q3ECTH.
PIR; B33276; B33276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y868_HAEIN STANDARD; E Q57022; P96336; I5-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last seq. 15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                         40524 MW;
                                                                                                                                                                                                                                                                                                                        75; Conservative
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                                                                                                                                                                                                                                                                        344 AA;
                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                        Complete proteome.
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                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                             "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIENAVDYDMF 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 IMSKP-NGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTN 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 -KLVTTSK-----KIDYLTLLQG------NQFKIMTVLVERESIKLLRFPNI- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 IPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVR 491
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Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D. Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.Fine L.D., Fritchman J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96; Indels 104;
                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFFTPTNQGPAAARNIGLEKAQGDYITFLDSDDFIANDKL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 AA; 28915 MW; A5D8220129782E98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.2%; Score 214; DB 1;
23.6%; Pred. No. 4.1e-05;
Lve 49; Mismatches 96;
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Minor teichoic acids biosynthesis protein ggaB.
GGAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32768; AAC22526.1; -.
HSSP; P39621; 1QGQ.
TIGR; HIO868; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.68;
                                                                                                                                                                                                                                                                                                     Science 269:496-512(1995).
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                                                                                                     RA Kunster, owequeure, and the state of the 
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1- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF GALACTOSAMINE-CONTAINING

NINGR TEICHOIC ACIDS.

1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 PIFFAEGRIGEHNLN-----NKFS----STRILDVEKEPHHILTHCCSTFIKKDALKN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 597 -- FNENIENAVDYDMF-LKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 SIYIPAYNCANYIQRCVDSALNQTV--VDLEVCICNDGSTDNTLEVINKLYG----NNPR 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 IVYAKKONGGVSSARNYGLKYAEGRYIQFLDPDDLVSEGTFENVLNFFDEHKNEIDIVAI 127
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21.3%; Pred. No. 0.00025;
.ive 94; Mismatches 240; Indels 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e; Glycosyltransferase; Complete proteome.
900 AA; 107154 MW; FA66495488C2C62F CRC64;
(AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SubtiList, BG11192, ggaB.
InterPro, IPR001173, G1ycos_transf_2.
Pfam, PF00535, G1ycos_transf_2; 1.
Transferase, G1ycosyltransferase, Com
                                                                                                MEDLINE=98044033; PubMed=9384377;
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            Submitted
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MEDLINE=90264305; PubMed=2111805;
Holland D., Wolk C.P.;
"Identification and characterization of hetA, a gene that acts early in the process of morphological differentiation of heterocysts.";
J. Bacteriol. 172:3131-3137(1990).
-: SIMILARITY: BELONGS TO THE GLXCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                    261 MVMHDLKWKLLIKDISETPLDENEYSEFLTLIREVLSYIDDDVIIE--TKSVSHFYLYHA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378 LFNSKGFKFYAKIGETKIKAKNIKRQHNDYISLGEVIKKYPGFSIDIPKGHLADNHHIEF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---QFALLILEKKTGH-----------------VFNKTSTLTYMPWERKLQWTN 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 FIKEFRFLKSLHKSGEKSKKRKSALKKALMARWVHHVFTIFNRKPVWLFIDRQDKADDNA 551
                                                                                              QSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYP 713
                                                                                                                                                                                                                                                                                                                                                                                  813
714 NTLNGLVKKL------NNIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKHQ
                                                                                                                                                                                                                                                                                                                                                                               762 VNILLNNDISYYTSNRLIKTEAHLSN----INKLSQLNLNCEYIIFDNHDSLFVKN----
                                                                                                                                                                                                                                                                                                                                                                                                                       -----DSYAYMKKYDV-GMNFSALTHDWI---EKINAHPPFK-KLIKTYFNDN-DLRS
                                                                                                                                                               ----ITFSKNL-----IDIIKNHEQKIPLFLQY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNVKGASQGM----FMKYA-LPHELLTIIKEVITSCQSIDSVPEYNTEDIWF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1991 (Rel. 19, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative glycosyl transferase alr2836 (EC 2.-.-).
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                                                                                                                                                                                             234 HSL-----
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01-NOV-1997
01-NOV-1997
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Guo D., Bowden M.G., Pershad R., Kaplan H.B.;
"The Myxococcus xanthus rfbABC operon encodes an ATP-binding cassette transporter homolog required for O-antigen blosynthesis and multicellular development.";
J. Bacteriol. 178:1631-1639(1996).
-i- FUNCTION: INVOLVED IN O-ANTIGEN BIOSYNTHESIS.
                                                                                                                                                                                                                                             FQANQGQGGAFNAGFAAATGEVVAFLDADDVWKPHKLQRIVEVFQTSDVVGVMHHLDIID 122
                                                                                                                                                                                                                                                                       -KDKTLACVYTTNRNVNPD-GSLI----ANGYNWP-----EFSREKLTTAMIAHHFRMFTI 588
                                                                                                                                                                                                                                                                                         -----KKLGIQKKNHFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEE 689
                                                                                                                                                                                                                                                                                                                                                                                                    SATSEQEAKSQAGIEMTNQY--INDFLVRIGYG-----ARVDLSRNLQYRRTKYYQRS 270
                                                                                                                                                             435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNP-RVRIM 493
                                                                                                                                                                                     3 ISVIISNYNYARYLSRAINSVLAQTHSDIEIVIVDDGSTDNSRDVITQLQEQAPDKIKPI 62
                                                                                                                                                                                                                                                                                                                             ----RAWHLTDGFNENIENAVDY-DMFLKLSEVGKFKHLNK-ICYNRVLHGDNTSI---
                                                                                                          Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                      Match 3.9%; Score 199.5; DB 1; Length Local Similarity 26.4%; Pred. No. 0.00034; les 81; Conservative 48; Mismatches 101; Indels
            PIR; B35391; B55391.
InterPro; IRPOIT3; Glycos_transf_2.
Pfam: PF00555; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                               322 AA; 36388 MW; 753C2FB59327D968 CRC64;
                                                                                                                                                                                                                  SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
0-antigen blosynthesis protein rfbC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1275 AA.
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InterPro: IPR001296; Glycos_transf_l.
InterPro: IPR001173; Glycos_transf_2.
Pfam: PF00534; Glycos_transf_l: 1.
EMBL; AF031959; AAC32401.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myxococcus xanthus.
                                                                  Complete proteome. SEQUENCE 322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-DK6640;
                                                                                                                                                                                                                                                                                                                                                                                                                                       690 MDMLKDL 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 QWDLREV 277
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                                                                                                          Query Match
                                                                                                                                  Matches
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                                                                                                                                                                                                       14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       720 VKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILA--FYHKHQVNILLNND----- 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      570 -----VRGTPKVSIIVPFKDRPDLLRTLVDSLLAQTRYPHFEVLLVSNNSTRPETFAL 622
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                                                                                                                                                                                                                                                                         427 SHIHRIPLVSIYIPAYNCAN-YIQRCVDSALNQTVVDLEVCICNDGST-DNTLEVINKLY 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433 ALLYTDEDGLDAQGHRSAPFFK-PDWSPDLLRSVDYVRHFLVVRRETLAQVGGLREGFDG 491
                                                                                                                                                                                                                                                                                                                485 GNNPRVRIM-SKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 ERESRIRVLTASSEGDTARATNEGFAACRGDFVGFLGAEDTLSPHALAEVALAFLAQPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544 ACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 604 AVDYDMFLKLSE-VGKFKHLNKICYNRVLHGDNTSIKK---LGIQKKNHFVVVNQSLNRQ
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                                                                                                                                                                                                       71;
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                        Length 1275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2. STRONG, TO M.GENITALIUM MG025.
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                                                                                                                                                                                                       Indels
Pfam; PF00535; Glycos_transf_2; 2.
Lipopolysaccharide biosynthesis.
SEQUENCE 1275 Aa; 139596 WW; 3AF9662A10A140F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last annotation update)
Putative glycosyl transferase MG025 homolog (EC 2.-.-.)
(B01_orf299V).
MPN028 OR MP126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         770 ISYYTSNRLIK-TEAHLSN---INKLSQLNLNCEYIIFDNHD 807
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35, Last sequence update)
40, Last annotation update)
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InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
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MEDLINE-97105885; PubMed-8948633;
                                                                                                                                                                                                          84; Conservative
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                                                                                                                                                                       Best Local Similarity
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EX5B_BUCAI
P57529;
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ID EX5B_BU
AC P57529;
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A Kunst F., Ogsawara N., Moszer I., Albertini A.M., Alloni G.,
A Zevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
A Zevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
A Zevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
Borise R., Boursehi C.V., Caldwell B., Capuano V., Carter N.A.,
A Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
A Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,
A Britan K.D., Errinford J., Fabret C., Ferrari E., Foulger D.,
A Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Fritz C., Fujita M., Fujita Y., Harwood C.R., Henaut A.,
A Gliseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
A Gris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A Nobyashi Y., Koetter P., Kohingstein G., Krogh S., Kumano M.,
Kunita K., Levine A., Lardinois S., Lauber J., Lazarevic V.,
A Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
A Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
A Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
                                                                                     10;
                                                                                                                                                                                                                                                          --YISPKRRFELKPYFGKTGVIEOKTKLRTPHSQPLAKFYRHEIFHLLDPLKEKL---FY 179
                                                                                                                                                                                                                                                                                                                    217
                                                                                                                                                                                                                               550 NRNVNPDGSLIANGYNWPEFSREKLTTAMIAHH---FRMFTIRAWHLTDGFNENIENAVD 606
                                                                                                                                                                                                                                                                                         661
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                                                                                                                                                                                                  66 YLEKPNGNWGSVVNFVKQNQLAKGQYITVLDSDDYFLANAFQRVAAHFGHDMIVSAFYC- 124
                                                                                                                434 LVSIYIPAYNCANYIQRCVDSAL -- NQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVR 491
                                                                                                                                  6 LFTVIIPTYNCGQYIPKALDSLLLQGEXFTKTQVLIVNDGSTDNTKQIVEPYTQQYSNIE 65
                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                               (FDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYPNTLNGLVK
                                                                                                                                                                        492 IMSKPNGGIASASNAAV--SFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTT
                                                           DB 1; Length 299;
                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Freymond P., Karamata D.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
 Hypothetical protein; Transferase; Glycosyltransferase;
                Complete proteome.
SEQUENCE 299 AA; 34935 MW; 9A3AF2F099283565 CRC64;
                                                                                                                                                                                                                                                                                                           180 QDCLLTHNAINKVQSVFYICEPLAVWYATRPGNSTTMP-----
                                                         3.8%; Score 193.5; DB 1;
24.5%; Pred. No. 0.00066;
tive 38; Mismatches 127;
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15-JUN-2002 (Rel. 41, Last annotation update)
Minor teichoic acids biosynthesis protein ggaA.
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101-NOV-1995 (Rel. 32, Last sequ
15-JUN-2002 (Rel. 41, Last anno
                                                                                         Conservative
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SEQUENCE FROM N.A.
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                                                                           Similarity
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                                                                 Local St. 74;
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P46917;
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GGAA_BACSU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                       Nature 390:249-256(1997).
-!- FUNCITON: INVOLVED IN THE BIOSYNTHESIS OF GALACTOSAMINE-CONTAINING
-!- FUNCITON: LINOLORDED IN THE BIOSYNTHESIS OF GALACTOSAMINE-CONTAINING
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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   Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Satolian E., Schleich S., Schroeter R., Scoffone F., Sekjuchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Sorokin A., Tanakoshi A., Tanakashi H., Tarepstra P., Tognoni A., Togato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Walizeneger T., Viari A., Wanhat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zumatein E., Yoshikawa H.F., Zumatein E., Yoshikawa H. Danchin A.; The complete genome sequence of the Gram-positive bacterium Bacillus
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Subtilist; BG11367; ggaA.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Transferase; Glycosyltransferase; Complete proteome.
SEQUENCE 446 AA; 53148 MW; BB369BD9B6856C42 CRC64;
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; Pred. No. 0.0014;
69; Mismatches 136;
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Matches 99; Conservative
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949 GKKTGLMIHYILKNLHVLKNKNSNWFSCILEKYNIHIK---WTSVLIYWIKNINTPLND 1005
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STRAIN-ATCS 35210 / B31;
STRAIN-ATCS 35210 / B31;
STRAIN-ATCS 35210 / B31;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artlach P., Bowman C.,
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Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
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   476 PVVPSSKNLKMNFTINDVAQT---
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                                                                                                                                                                                                                                                                                                                                                                      MEDINE-20445173; PubMed-10993077;
Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Selomber Sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Nature 407:81-86(2000).
-! FUNCTION: REQUIRED FOR EFFICIENT DNA REPAIR; IT CATALYZES THE
-! FUNCTION: REQUIRED FOR EFFICIENT DNA AND THE CLEAVAGE OF SINGLE-
STRANDED DNA AND IT STIMULATES LOCAL GENETIC RECOMBINATION. ALL OF
THESE ACTIVITIES REQUIRE CONCOMITANT HYDROLYSIS OF ATP (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;
DNA repair; Complete proteome.
NP_BIND 25 31 ATP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 PSITSKGNISLDWRLEHFKKTDNLRLCDSPFRYFVAGNVAFS----KEWLNKVGWFDEEF 356
                                                                                                                                                          Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 SNVKKLTLSESEKNSLKNKW-KSITGKKSENAEIRKVELVPKDFPKDLVLAPLPDHVNDF 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 DEFQDTDIQQY-KIFNLLYKKNKTTVLFL------IGDPKQAIYSFRGAD-----IF 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Exonucleolytic cleavage (in the presence of ATP) in either 5'- to 3'-or 3'- to 5'-direction to yield 5'-phosphooligonucleotides.
SUBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 NDLEINKKIYSK-----FNLIKWINK----ITEWAKSETKDYIIP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 TWYKNRKKSLGIKPVNKNIGLSIIIPTFNRSRIL-DITLACLVNQKTNYPFEVVVADDGS
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Matches 200; Conservative 172; Mismatches 348; Indels 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE HELICASE FAMILY. UVRD SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.7%; Score 189; DB 1; Length 1174; 18.6%; Pred. No. 0.0067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 347 POLY-LYS.
1174 AA: 139037 MW; 668FE1336F1F190A CRC64;
                                                                                                                                                                       symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBL_TaxID=118099;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Exodeoxyribonuclease V beta chain (EC 3.1.11.5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-TOkyo 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                            RECB OR BU454.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;
DNA repair; Complete proteome.
NP_BIND 18 25ATP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390 PPGKENETEREAGKSITLKIVKEKVPYIYRKLLPIEDSHIHRIPLVSIYIPAYNCANYIQ 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----IYHKEQNIQSLIS 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDARIVLKINHRSSKKLIG--PLNKIFNNIYNNAIADEIEK---IDFINS-LPNQKNDNN 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 WKSITGKKSENAEIRKVEL--VPKDFPKDLVLAPLPDHV-----NDFTWY----KNR-- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 YKIILIDEAQDLSLIQIEIFKILKTAGIKLIFIADPKQIIYSFRKADISFYNKEIKNKIN 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KKSLGIKPVNK---NIGLSIIIPTFNRSRILDITLACLVNQKTNYP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.6%; Score 183; DB 1; Length 1169;
19.3%; Pred. No. 0.014;
.ive 138; Mismatches 321; Indels 272; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 VEFQIIKCKEKLSTNSYVSEDKKNSVCDSSLDIATQLLLSNVKKLTLSESEK--NSLKNK 92
                                                                                                                   FUNCTION: REQUIRED FOR EFFICIENT DNA REPAIR; IT CATALYZES THE UNWINDING OF DOUBLE-STRANDED DNA AND THE CLEAVAGE OF SINGLE-STRANDED DNA AND IT STIMULATES LOCAL GENETIC RECOMBINATION.
ALL OF THESE ACTIVITIES REQUIRE CONCOMITANT HYDROLYSIS OF ATP (BY SIMILARITY).
CATALYTIC ACTIVITY: Exonucleolytic cleavage (in the presence of ATP) in either 5'- to 3'- to 5'-direction to yield 5'-
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Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
SIMILARITY: BELONGS TO THE HELICASE FAMILY. UVRD SUBFAMILY.
                                                                                                                                                                                                                                                                                                  phosphooligonucleotides.
SUBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECD
                                               sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).
IW; B61D63C1C959B91F CRC64;
  Horst K.,
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Interpro; IPR000212; UvrD-helicase.
     Cotton M.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001164; AAC66981.1; -.
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                                                                              burgdorferi.";
Nature 390:580-586(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 1169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P56255; 1PJR.
BB0633; -.
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Matches 175; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .002 TRLCDIEELQKEMEFLIKINPEFQKQ------KYLFDKHFEDLHIKLSDGYLKGIVDLI 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1055 FRANNKIYILDYKTN-----YLGKNKEDYNITNLENTIKKEYYDLQYKIYALGIKKILF 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNK---DAKIAVSIFYPNTLNGLV 720
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RCVDSALNQTVVDLEVCICNDGSTDNTLEVI----NKLYGNNPRVRIMSKP--NGGIASA
                                                   TLESLIINEEPEEIEEKINNINNDNESIELMTIHKSKGLGMNIVFLLNTTPIENSNFFSK
                                                                                                                                      826 ITSKLLEIAKIFTIDDIKHDFNIHEFIGQKRFNKKKYNTNVNTKLIPPKPIIKNMFK-KE
                                                                                                                                                                                                                                                                                                                           FSREKLTTAMIAHHFRWFTIRAWHLTDGFNENIENAVDYDWFL-----KLSEVGKFKH--
                                                                                                                                                                                                                                                                                                                                                                                    YTSSFSSLTAQAHHKEFYENYDF---KNINYEKETELDYEPGLEETLPKGKDIGNILHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                        LNKICYNRV-----LHGDNTSIKKLGIQKKN---HFVVVNQSLNRQGINYYNYD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa "Genome sequence of the endocellular bacterial symbiont of buchoars on abc ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                          SNAAVSFAKGYYIGQLDSDDY-LEPDAVELCLKEFLKDKTLACVYTT----
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TRANSMEM 12 32 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID=118099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
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Buchnera sp. APS.";
Nature 407:81-86(2000).
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MEDLINE-20445173; PubMed-10993077;
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P57189;
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative glycosyl transferase MG025 (EC 2....).

298 AA

PRT;

STANDARD;

RESULT 13 Y025_MYCGE ID Y025_MYCGE ST AC P47271; Q49359;

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                                                                                                            [1]
SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLIND-96026346; PubMed-7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischman R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small R.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
The minimal gene complement of Mycoplasma genitalium.";
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Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE OF 172-298 FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-4075230; Pubmed-8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing.";
J. Bacteriol. 175:7918-7930(1993).
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY
STRONG, TO M.PNEUMONIAE MPN028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
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298 AA; 35044 MW; B7BCCC73EB2CA023 CRC64;
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EXEN_CLOBU STANDARD;

006366;

01-FEB-1995 (Rel. 31, Created)
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BXEN_CLOBU
ID BXEN_C
AC Q06366
DT 01-FEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
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-----PNTLNGLVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKHQVNIL 765
                          214 TITSWENPNKFNAWCEILQKMNLYGAGIVIYIY-----TMLPGFLKQL----KKKQLILN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          + {DNA}(N).
--- SUBCELULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C FAMILY. POLC SUBFAMILY.
                                                                                                                                                                                                                                                       Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 407:757-762(2000).
-!- FUNCTION: REQUIRED FOR REPLICATIVE DNA SYNTHESIS. THIS DNA
POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5%; Score 176; DB 1; Length 1442;
llarity 17.9%; Pred. No. 0.045;
Conservative 176; Mismatches 378; Indels 38
                                                                                                                                                                                                                                                                                                                                                        Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                      complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase; DNA-directed DNA polymerase; DNA replication Nuclease; Exonuclease; Complete proteome.

MoMAIN 409 575 EXONUCLEASE.

SEQUENCE 1442 AA; 166227 MW; 834(35E722ACA6D1 CRC64;
                                                                                                                                                                                           15-UN-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
DNA polymerase III polC-type (EC 2.7.7.7) (PolIII).
POLC OR UU377.
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                                                                                                                                                             1442 AA.
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MEDLINE=20500219; PubMed=11048724;
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InterPro; IPR000520; Exonuclease.
InterPro; IPR003141; PHP_N.
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                                                                                                                                                                                      (Rel. 40, Created)
(Rel. 40, Last seq!
(Rel. 41, Last anno
                                                                                                                                                             STANDARD;
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Matches 204; Conserv
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LNHKPAY 271
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830 ALTHDWIEKI-------NAHPPFKKLIKTYFNDNDLRSMNVKGASQGMF 871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                746 TPDIKKEILAFYHKHQVNILLNNDISYYTSNR-----LIKTEAHLSNINKLSQLNL--- 796
                                                                                                                                                                                                                                                                                                                                                                366 FGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKEKVPYIYRKLLPIE 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               557 ADYDAIVLADVFKVMKNNLFNDFGITNLSEINTKLOTTMLKNRSFGNMINLYIKNOANVK 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       607 YDMFLKLSEVGKFKHL------NKICY-----NRVLHGDNTSIKKLGIQKK 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RYDFITLPSLGSQKHLVYAKKITIENVQKAFKKLIYLALELNKIIIYSSSPYYFFKDDKK 736
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                                                                                                                                                                                                                                             LIDFAVKNQLKTIG-----KPSKKQDLKIIY 382
| | | | | | | | 334
                                                                                         ----KTTH 1074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAKIAVSIF-----YPNTLNGLVKKLNNIIE-----YNKNIFVIILHVDKNHL
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                                                                                                                                   KYVRQKDYGY-----QLCAVRNLGLR---TAKYDF----VSILDCDMAPQQLWVHSY
                                                                                                                                                                                                              LTELLEDNDIVLIGPRKYVDTHNITAEQFLNDPYLIESLPETATNNNPSITSKGNISLDW
                                                                                                                                                                                                                                                                                                                                                                                                                                           426 DSHIHRIPLVSIYIPAYNCANYIQRCVDSALNQ-----TVVDLEVCICNDGSTDNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    525 LEPDAVELC------CVYTTNR-NVN
                                                                                                                                                                                                                                                                                       314 RLEHFKKTDNLRL------CDSPFRYFVAGNVAFSKEWLNKVGWFDEEFNHWGGEDVE
                                                                                                                                                                                                                                                                                                                -----IIEFGAVIMQNN-------KQIGEKIQFFIKPIQQIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVINK---LYGNNPRVRIMSKPNGGIASASNAAVSFAKGYYIGQL------DSDDY
                                                          --IVQKYEQKLDI
                                                                                                                                                                  289 VLDNMSKSGQVPIGKIKKICCVEDKHVKKQITPRLELNFHTKMSSLDAIISTQE-----
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                                                            LDITLACLVNQKTNYPFEVVVADDGSKENLLT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 YFKNYNINGF-----KNG-----QIKTKLPLSKYNKEIINKPELIVNLINQNNTVLMKS 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KNSLKNKWK------SITGKKSENAEIRKVELVPKDFPKDLVLAPLP 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 AEQF - LNDPYLIE - - - - SLPETATNNNPSITSKGNISLDWRLEHFKKTDNLRLCDSPF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 NYIANSIKLYLEQKFKINVKDIWELNLSYFSKEFQIMMPERYNNALNHYYRK--EFYVID 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----FEVVVADDGS-----KENLLTIVQ---KYEQKLDIKYVRQKDYGYQL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             471 AOMIDSNDINLSSDFLKVISSKGSLVYSFLNNTMDYLEFIKYDKPID---TDKKYYKWLK 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        570 VEEFKNLGPIFLINKKENITIPKIKIDEIPS--SMLNFS-----FKD-----LSENLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 NFYGDGLKGNVDNFYSNYIIPYNLNYEHSINYSYLDNVNIEEIEKIPP------
                                                       Clostridium butyricum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                    Fujii N., Kimura K., Yokosawa N., Oguma K., Yashiki T., Takeshi K., Obyama T., Isogai E., Isogai H.; Simiarity in nucleotide sequence of the gene encoding nontoxic component of botulinum toxin produced by toxigenic Clostridium butyricum strain BL6340 and Clostridium botulinum toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.4%; Score 175.5; DB 1;
llarity 19.5%; Pred. No. 0.036;
Conservative 137; Mismatches 322;
Ol-NED-1995 (Rel. 31, Last sequence update)
Ol-NOV-1995 (Rel. 32, Last annotation update)
Botulinum neurotoxin type E, nontoxic component.
Clostridium butyricum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000395; Bontoxilysin.
Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00766; BONTOXILYSIN.
ProDom; PD001963; BONTOXILYSIN; 1.
                                                                                                                                                       STRAIN-BL6340;
MEDLINE-93360835; PubMed-8355622;
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Matches 202; Conserv
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                         NCBI_TaxID=1492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :| :: | :: | | :: | 883 KLIGSKEDNCGWEIYFENNGLVFNIIDSNGNEKNIYLSNIS-----NKSWHYIVISINRL 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   938 KDQLLIFIDNILVANEDIKEILNI-YSSDIISLLSDNNNV--YIEGLSVLNKTINSNEIL 994
PGKENETEREAGKSITL--KIVKEKVPYIYRKLLPIEDSHIHRIPLVSIYIPAYNCANYI 448
                                                                                                                                     -----LEVCICNDGSTDNTLEVINKLYGN 486
                                                                                                                                                                                                                                                                                                                                                     NETEKSHLIMON-----SFSNLDFDFLDIQNMKNLFNLYTELLIKEQTSPYELSLYAFG 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------AIHLT-GANQNIKETNDY-----FENGLINFSIYFWLRNLNQNTIKS
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                                                                                                                                                                                                                                                                                  ---GXXIGO
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                                                           ------ASKSVLAQEKLIKKLIQKQLRYLM--ENSNISSTNLILINLTTTNTLRDI
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1 MNTLSQAIKAXNSNDYELAL......SAKKGENIPVNKFIINSITL 965
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Perfect score:
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1: sp_archea:*
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4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_cyanelle:*
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:*
11: sp_vertebrate:*
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14: sp_unclassified:*
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_21:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O9ki99 pasteurella	Q9cmp0 pasteurella	Q9ahl6 pasteurella	085457 pasteurella	068389 pasteurella	092if9 rickettsia	Q8y828 listeria mo	Q9clr9 pasteurella	Q9als8 campylobact	Q8xn37 clostridium	O88090 enterococcu	Q97p72 streptococc	Q8xn34 clostridium	Q8ys17 anabaena sp	Q9k616 bacillus ha	086893 streptococc
SUMMARIES	ID	09кл99	5 Q9CMP0	Q9AHL6	085457	068389	5 Q92IF9	5 Q8Y828	5 Q9CLR9	Q9ALS8	5 Q8XN37	088090	5 Q97P72	5 Q8XN34	5 Q8YSL7	5 Q9K6L6	086893
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Gaps

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Mismatches

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Matches 965; Conservative

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121 VLAPLPDHVNDFTWYKNRKKSLGIKPVNKNIGLSIIIPTFNRSRILDITLACLVNQKTNY 180

258.5 5.1 342 16 08XN 256.5 5.1 333 16 097H 256.5 5.1 333 16 097H 256.5 5.1 333 16 097H 256.5 5.0 330 16 08XN 254.5 5.0 330 16 08XN 255.0 331 2 08XH 254.5 5.0 332 2 08XH 254.5 4.9 283 2 08XH 254.5 4.9 283 2 08XH 254.5 4.9 283 2 08XH 254.5 4.7 284 2 08XH 254.5 4.7 333 2 08XH 254.5 4.7 334 2 08XH 254.5 4.7 334 2 08XH 254.5 4.7 335 2 08XH 254.5 4.7 336 2 08XH 255.5 4.6 1238 12 09EXH 254.5 4.6 1238 12 09EXH 255.5 4.6 1238 12 0	lostridiu lostridiu anabaena si lostridiu nabaena si reptococc reptococc reptococc reptococc reptococc reptococc reptococc	Quade leptospira	i.gonments ; 965 AA. ed) sequence update) annotation update) .ubdivision; Pasteurellaceae;	4; 50.; oning of a Chondroitin Synthase from 000). sf_2. AFCD55CD59D35C8C CRC64; AFCD55CD59D35C8C Length 965; ed. No. 8.1e-256;
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                                                               KTLACVYTTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRWFTIRAWHLTDGFNEN
                                              GEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKEKVPYIYRK
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PFEVVVADDGSKENLLTIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKYDFVSILD
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
NCBI_TaxID=747;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein PM0775.
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                                                                                                                                                             Length
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                                                                                                                                    CRC64;
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965 AA; 111600 MW; 9C4B2CF80E1A6BD7
                                                                                                                                                          94.4%; Score 4802; DB 16;
11arity 93.0%; Pred. No. 6e-241;
Conservative 42; Mismatches 26;
                                                                                    HSSP; P39621; 1QGO.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 2.
Pypothetical protein; Complete proteon
SEQUENCE 965 AA; 111600 MW; 9C4B20
           STRAIN=PM70;
MEDLINE=21145866; PubMed=11248100;
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FROM N.A.
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MEDLINE-98442423; PubMed-9770287;
Chung J.Y., Zhang Y., Adler B.;
The ospaile blosynthetic locus of Pasteurella multocida
FEMS Microbiol. Lett. 166:289-296(1998).
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF067175; AAC67250.2; -.
HSSP: P39621; 10GQ.
InterPro: IRR01173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2.
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085457; OB5457;
01-NOV-1998 (TrEMBLrel. 0
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Glycosyl transferase.
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                    NTEDIWFOFALLILEKKTGHVFNKTSTLTYMPWERKLOWTNEQIOSAKKGENIPVNKFII
                                                                                              GEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKEKVPYIYRK
  AHPPFKKLIKTYFNDNDLRSMNVKGASQGMFMKYALPHELLTIIKEVITSCQSIDSVPEY
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Pasteurella.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                AA.
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Pfam; PF00535; Glycos_transf_2; 2.
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MEDLINE-21142635; PubMed-11230405;
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                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Pasteurella multocida
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SEQUENCE 9
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                             TSNRLIKTEAHLSNINKLSQLNLNCEYIIFDNHDSLFVKNDSYAYMKKYDVGMNFSALTH
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                                                                                         VNQKTNYPFEVVVADDGSKENLLTIVQKYEQKLDIKYVRQKDYGYQLCAVRNLGLRTAKY
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                     MNTLSQAIKAYNSNDYELALKLFEKSAETYGRKIVEFQIIKCKEKL----STNS
ed. No. 5.9e-225;
Mismatches 60;
  Pred.
 86.88;
        844; Conservative
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   Similarity
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STRAIRS-P-1059, AND ATCC 15742;
MEDLINE-98192645; PubMed-9555958;
DeAngelis P.L., Jing W., Drake R.R., Achyuthan A.M.;
Identification and modecular cloning of a unique hyaluronan synthase
from Pasteurella multocida...;
J. Blol. Chem. 273:8454-8458(1998).
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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86.6%; Pred. No. 1.4e-224;
tive 63; Mismatches 60;
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hes 842; Conservative
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01-JUN-2002 (TrEMBLrel.
Hyaluronan synthase.
                                  01-AUG-1998 (TrEMBLrel. 01-AUG-1998 (TrEMBLrel.
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A Glaser P., Frangeul L., Buchteser C., Rusniok C., Amend A.,

A Glaser P., Frangeul L., Buchteser C., Rusniok C., Amend A.,

A Glaser P., Frangeul L., Buchteser C., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Demoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

B Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

A Gautier L., Goebel W., Gomez-Lopez N., Hauf J., Jackson D.,

A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

A Moueno E., Maitouram A., Mata Vicente J., Ng E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simoss N., Tierrez A.,

A Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

Comparative genomics of Listeria species.";

Science 294:849-852(2001).

Comparative Genomics of Listeria species.";

Listilist; LMO01090;

InterPro; IPR001173; Glycos_transf_2.

R Pfam; PF00535; Glycos_transf_2.

R Pfam; PF00535; Glycos_transf_2.

SEQUENCE 327 AA; 37843 MW; F7480656043EC2FC CRC64;
                                                                                                                                                                                                                   386 K-DKIEIQLKFMEENNF-IFSHTSYHKINE-------KGKYIESVHSGLF 426
                                                                                                                                                                                                                                                                                               347 KRIKYFHK--------KNEGPAAARN-LGIKNAIGKYIAFLDSDDLFY 385
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                    234 ECNVLWSSFLHELTEEEMIKMEGSPYL-----FLTRTATFLSNNT-PYKKACDLANTWA
                                                                                                                                                                                                598 LIQNKDAKIAVSIFYPNTLNGLVKKLNNI-IEYNKNIFVIILH----VDKNHLTPDIKKE
 LKEFLKDKTLACVY - - - - - TTNRNVNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMF
                                                                 587 TIRAWHLTDGFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKK
                                                                                                 175 PAKYFHEVGIFNEALPTTQDYDLWFKIFRVAPIHFDESILIKSRFHSEQGS-KKISNHNE
                                                                                                                                  547 N------HFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLK
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein lmo1090.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.7%; Score 292.5; DB 1
27.5%; Pred. No. 7.7e-08;
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STRAIN-EGD-E / SEROVAR 1/2A;
MEDLINE-21537279; Pubmed-11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                     872 MKYALPHELLTIIKEVITSC
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                  953
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                                                                                 TOGENEKIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNYSIKKLGIQKKNHFVVVN 660
                                                                                                                                                                                                                                                                                                                                  893
                                                                                                                                                                                                                                                                                                                                                  EVINKLYGNNPRVRIMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVE----LC 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | |: || || || || || || ERVALSYGD--KIRYEYKENGGCGSALNYGIKNMQGEYFSWLSHDDIYYPNKIEHQVDIL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKLLPIEDSHIHRIPLVSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDN-TL 477
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EMBL, ARD03699; AAL02991; -.
InterPro; IPR001173; Glycos_transf_2.
Pfam, PR00355; Glycos_transf_2.
Fransferase: Hypothetical protein; Complete proteome.
SEQUENCE 604 AA: 69121 MW: 514CDD81DC3FB3AB CRC64;
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                   TDGFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN
                                                                                                                                QSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIAVSIFYP
                                                                                                                                                                                                NTLNGLVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKHQVNILLNNDISYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=MALISH 7;
MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92;
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=781;
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Last annotation update)
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24.8%; Pred. No. 1.3e-07;
tive 71; Mismatches 213;
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01-DEC-2001 (TrEMBLEel. 19, Last sequenc
01-MAR-2002 (TrEMBLEel. 20, Last annotat
Putative two-domain glycosyltransferase.
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Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 INNEENKGFIASLNIGIASINGDYLARTDADDITKPEWIEKILGYMLSHPQIIAMGSYLT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                550 NRNVNPDGSLIANGY----NWPE-FSREKLTTAMIAHH------FRMFTIRAW 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----YEESKDQLAYLYIEHLIYRLVL 249
                                                                                                          174 VILKAKNPVKIQDALYYXITDRADSQSNIQQVDHFLDVVI--MLENVETELKKLGI---- 227
                                                                                                                                 HFVVVNQSLNRQGINYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDL---KLIQNKDA 704
             -----NENIENAVDY----DMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKN 647
                                                                                                                                                                                                                                                                                                                                                                                                                         May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL; AB006155; AAK03224.1; -.
Interpro, IPR001173; Glycos_transf_2.
Pfam; PF00555; Glycos_transf_2.

Ppam; PF00555; Glycos_transf_2.

ERQUENCE 337 AA, 39267 MW; 8639BGFB5F700DB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLTDGFNENIENAVDYDMFLKLSEVGKF-KHLNKICYNRVLHGDNTSIKKLGIQKKNHFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVNQSLNRQGINYYNYDKFDDLDESRK----YIFNKTAEYQEEMDMLKDLKLIQNKDAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 LMAKKIRKRAINYY----LQDLGVIHRLGEDIFFHDIETIQAE---LASLSLLDN---CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   707 AVSIFYPNTLNGLVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKHQ 761
  193 MSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNRN
                                            VNPDGS-----LIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGF---
                                                                                                                                                                             KIAVSIFYPNTLNGLVKKLNNIIEYNKNIFVIILHVDKNHLTPDIKKEILAFYHKH 760
                                                                                                                                                                                              Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
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                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein PM1140.
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27.0%; Pred. No. 8.5e-08;
ative 67; Mismatches 124;
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                                                                                                                                                                                                                                                                PRELIMINARY;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        661 I-------NYYNYDKFDDLDESRKYIFNKTAEYQEEMDMLKDLKLIQNKDAKIA 707
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                                                                                                                                                                                                             Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493 MSKPNGGIAS-ASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYT---
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                                                                                                                                                                                                                                                                                                                                           STRAIN-NCTC 11828;
Oldfield N.J., Millar L.A., Ketley J.M.;
"Gene content polymorphisms in Campylobacter jejuni LOS clusters".
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF343914; AR12955.1; InterPro; IPR001173; Glycos_transf_2. Pfam; PF00535; Glycos_transf_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 350 AA; 41616 MW; FB19017F89326E9E CRC64;
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                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical 41.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.6%; Score 287.5; DB 2;
25.5%; Pred. No. 1.5e-07;
tive 66; Mismatches 129;
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    1 | 1 : 1 | 1 : 284 IKRILYDCYLSLVDNKLINILYFLR-
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Best Local Similarity 25.55
Matches 105; Conservative
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Pfam; PF00535; Glycos_transf_2;
PRINTS; PR00030; HTHCRO.
                                 706
80401 MW;
                                                                5.4%;
                                                                                                                       PRELIMINARY;
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                                          706 AA;
                                                                          Local Similarity
                                706
                     Transferase.
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SEQUENCE
                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      684 AEYQEEMDMLKDLKLIQNKDAKIAVSIFYPNTLNGLVKKLNNIIEYNKNIFVIILHVDKN 743
                                                                                                                                                                                                                                                                            495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNRNVN 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                                                                                                                                                                                                                             Gaps
                                                               Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     088090;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative glycosyl transferase (Fragment).
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                              579 -IAHHFRMFTIRAWHLTDGFNENIENAVDYDMFLK------LSEVGKFKHLNKIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-OGIRF;
MEDLINE-98380380; PubMed-9712783;
Xu I., Murray B.E., Weinstock G.M.;
"A dluster of genes involved in polysaccharide biosynthesis from
                                                                                                                                                                                                          93;
                                                                                                                                                                                       Length 326;
                                                                                                                                                                                 5.5%; Score 2,23.6e-07;
25.2%; Pred. No. 3.6e-07;
.tive 66; Mismatches 114; Indels
                                                                                                                                                                326 AA; 38553 MW; 76503BF0B5DE1C03 CRC64;
                                                                                                                                                                                                                                                                                                                      555 P-----DGSLIANGYNWPEFSREKLTTAM----
                                                                                                          U.S.A. 99:996-1001(2002)
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Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           907
                                                                                             flesh-eater.;

Proc. Natl. Acad. Scil. U.S.A. 99:996-;

EMBL: AP003187; BAB80207 1; -

InterPro; IPR001173; Glycos_transf_2.

Pfam; PF00535; Glycos_transf_2; 1.

Complete protecome:

SEQUENCE 326 AA; 38553 MW; 76503Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Entérococus faecalis OGIRF.";
Infect. Immun. 66:4313-4323(1998).
EMBL. AF071005; AAC35930.1;
InterPro; IPR001173; Glycos_transf_2.
InterPro; IPR000655; HTH_Cro.
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                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                 Local Similarity
                           SEQUENCE FROM N.A.
STRAIN-13 / TYPE A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1351;
           NCBI_TaxID-1502;
                                                     PubMed-11792842
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Matches
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088090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 ILEEIGGFRKGYEGSQDYDLVLRFTEKTTKERITHIPKVLYYWRMLPTSTAVDQGSKGYA 398
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                                                                                                                                                                                                                                                                                                               ------LEHFKKTDNLRLCDSPFRYFVAGNVAFSKEWLNK-----VGWF 352
                                                                                                                                                                                                                                                                                                                                                                                                                                               DEEFNHWGGEDVEFGYRLFAKGCFFRVIDGGMAIHQEPPGKENETEREAGKSITLKIVKE 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKVTRLW-----IKAKKGFKYMAKNGIS-HTIQRAKIEKLRNQA--SYPNWLARN 161
                                                                                                                                                                                                                                                                                                                                                                             60 NQIYQTEPAIEAGFVVTLEGIKQKKVL----PFHFQSSAHVVTVDFPLNKKYPVIPGTE 114
                                                                                                                            Gaps
                                                                                                                                                                                                                              2 NEDIKVIFDSIYRDKTINNLTITGWALDTITKES--PTFTINNENQVSAYNIQRVLREDV 59
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Bacteria: Firmicutes: Bacillus/Clostridium group; Lactobacillales; Streptococcacaes: Streptococcaceae: Streptococcacaes: NCBL_TaxID=1313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        590 AWHLTDGFNENIENAVDYDMFLKLSE---VGKFKHLNKICYNRVLHGDNTSIKK--LGIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKNHFVVVNQSLNRQGINYYN-----YDKFDDLDESRKYIFNKTAEYQEEMDMLKDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              488 AEFEQOLPGRFFVESIDIPF-----NFSTINNRAAKKAHGEYLLFLNNDTEVIT
                                                                                                                        Indels 167;
                                                                                                                                                                                          260 DNDIVLIGPRKYVD--THNITAEQFLNDPYLIESLPETATNNNPSITSKGNISLDWR-
                                                          DB 2; Length 706;
8710AD60C7D36315 CRC64;
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                                                              Score 276.5; DB Pred. No. 1.3e-06
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                                                 Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Reldblyum T.V., Andiuoli S., Dickinson T., Hickey E.K., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          745 LTPDIKKEILAF-----YHKHQVNILLNNDISYYTSNRLIKTEAHLSNINKLSQLNL 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 WIKOLNKRLEKFDSEIINCRVTSEQIS-CYKSDISYTVFLRYFIADF----VQEDKALYL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 DCDLVVTKNLDDLFATDLQDYPLAAVRDFGGRAYFGQEIFNAGVLLVNNAFWKKENMTOK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            686 YQEEMDMLKDLKLIQNKDAKIAVSIFYPNTLNGLVKKLNNIIEYNKNIFVIILHVD-KNH 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         552 N------VNPDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHL-- 593
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7 ITVIVPYYINVENYLRKCLDSIITQTYKNIEIVVVNDGSTDASGEICKEFSEMDHRILKIE 66
                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                          DB 16; Length 696;
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InterPro; IPR001495; GT_8.
InterPro; IPR002495; GT_8.
Pfam; PF00535; Glycos_transf_2; 1.
Pfam; PF01501; Glycos_transf_8; 1.
Fransferase; Complete proteome.
SEQUENCE 696 AA; 81336 MW; ADCA9C01AABB32C7 CRC64;
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                                                                                                                                                                                                                                                                                                       5.3%; Score 268.5; DB 16;
20.5%; Pred. No. 3.3e-06;
Live 96; Mismatches 181;
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                                          MEDLINE=21357209; PubMed=11463916;
                                                                                                                                                                     pneumoniae.";
Science 293:498-506(2001).
EMBL; AE007470; AAK75845.1; -
TIGR; SP1771; -
                                                                                                                                                                                                                                                                                                                    Best Local Similarity 20.5
Matches 101; Conservative
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                     SEQUENCE FROM N.A.
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787 NINKLSQLNLN----CEYI--IFDNHDSLFVKNDSYAYMKKYDVGMNFSALTHDWIEKIN 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           735 VIILHVDKNHLTPDIKKEILAFYHKHQ------VNILLNNDISYYTSNRLIKTEAHLS 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 --NKLYNIYREEFEYCVYIHNWYFRYRIIYFGNNQYS-KKLFEIWNNFNI-----SIR 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 QENRGSSEARKGYEMSTGEFILFVDGDDWIRNDTIEVLLE-----YS----N 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 EIQK----IWSLLYDK----INNEKIELRDTQFLREILTNNISIN-----IWNKF----I 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                 STRAIN-13 / TYPE A;
PubMed=11792842;
Shinizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shinizu T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              495 KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVELCLKEFLKDKTLACVYTTNRNVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    555 PDGSLIANGYNWPEFSREKLTTAMIAHHFRMFTIRAWHLTDGFNENIENAVDYDMFLKLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          615 EVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVNQSLNRQGINYNYDKFDDLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 348;
Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 NNKYFKKDEKNLDCYWRFFYLNAIN------NYYLGKILALIIK 331
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MEDLINE=21595285; PubMed=11759840;
Kaneko I., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 AA; 41769 MW; AE46C19FA8E52C93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Alr3067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae;
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.2%; Score 265.5; DB 16;
23.3%; Pred. No. 2.1e-06;
tive 68; Mismatches 132;
                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002)
EMBL, AP003187; BAB80210.1; ...
InterPro; IPR01173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Complete protecome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 23.33
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                          NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                    flesh-eater.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                          492 IMSKPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVEL---CLKEFLKDKTLACVYT 548
                                                                                                                                                                                                                                                                                                                                                                 127 YYKFANEADSYADESNSFAGDVYAELLIKNFLONGSN-PLIRRAAIDSVGL------ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       589 RAWHLTDGFNENIENAVDYDMFLKLSEVGKFKHLNK--ICYNRVLHGDNTSIKKLGIQKK 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 YSSIVIERAFNAAPPQLQHLKK-----QSLAWVYKFTAQQCLKYNSHKLADIKLAA-KRL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NHFVVVNQSLNRQGINYYNYDKFDDLDESRRYIFNKTAE--YQEEMDMLKDLKLIQNKDA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
EMBL: AP001519; BAB07432.1; -InterPro: IPR001173; Glycos_transf_2.
Pfam: PF00535; Glycos_transf_2; 1.
                                                                                                                                                                                                                                              61; Gaps
                                                                                                                                                                                                                                                                                              10 VPIISVIIPVYNGEKTIIETIASVQHQTFLDIEIIVINDGSTDNTFELVRNIQDN--RLK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
                                                                                                                                                                                                              DB 16; Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 261.5; DB 16; Length 303;
Pred. No. 2.8e-06;
                Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing Cyanobacterium Anabena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                             Query Match 5.2%; Score 264.5; DB 16; Length Best Local Similarity 25.4%; Pred. No. 2.1e-06; Matches 82; Conservative 64; Mismatches 116; Indels
                                                                                                            EMBL, AP003591, BABA766.1; -.
InterPro. IPR001173; Glycos_transf_2.
Pfam. PF00535; Glycos_transf_2, 1.
Hypothetical protein; Complete proteome.
SEQUENCE 323 AA; 36955 WW; 0AA1437F9EC42D89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C9F5471D29CD6076-CRC64;
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Last annotation update)
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MEDLINE-20512582; Pubmed-11058132;
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Bacillaceae, Bacillus.
NCBI_TaxID=86665;
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Q9K6L6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 KPL----VRYYNYTTNKQISDDIKKYESAIEYIDNKYVDLYSKVSEEIRRKHRHSMTMLI 252
                                                        435 VSIYIPAYNCANYIQRCVDSALNQTVVDLEVCICNDGSTDNTLEVINKLYGNNPRVRIMS 494
                                                                                                                                                                            495 -KPNGGIASASNAAVSFAKGYYIGQLDSDDYLEPDAVEICLKEFLKDKTLACVYT---- 548
                                                                                                                                                                                                                                                                                                   ---TNRNVNPDGSLIANGYNWPE----FSREKL-----TTAMIAHHFRMFTIRAWHLTD 595
                                                                                                                                                                                                                                                                                                                                                                                                                       --GFNENIENAVDYDMFLKLSEVGKFKHLNKICYNRVLHGDNTSIKKLGIQKKNHFVVVN 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           654 QSLNRQGINYYNYDKFDDL-DESRKY-----IFNKTAE----YQEEMDMLK 694
Gaps
                                                                                                                61
                                                                                          95;
95; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695 DLKLIQNKDAKIA----VSIFYPNTLNGLVKKLNNIIEY 729
60; Mismatches
Conservative
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